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                               phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome,
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                           present invention relates to Corynebacteium glutamicum
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium to producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                       Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                      Yokoi
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Ozaki A;
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Ikeda M,
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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AAH67869 standard;
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Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
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sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breads of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.

Sequence 5969 BP; 1388 A; 1575 C; 1578 G; 1428 T; 0 other;

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The present invention relates to Corynebacteium glutamicum phosphonolopyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome,
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                                                                                                                                                                               Length 1109
                                                                                                                                                                                                         Indels
                                                                                                                                        0 other;
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                                                                                                                                                                                 DB
                                                                                                                                          G; 292 T;
                                                                                                                                                                              Score 1107.4;
Pred. No. 0;
0; Mismatches
Page 103-104; 144pp; English
                                                                                                                                        Sequence 1109 BP; 236 A; 278 C; 303
                                                                                                                  transformation.
                                                                                                                                                                                                      ;
                                                                                                                                                                              72.5%;
llarity 99.9%;
Conservative (
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Matches 1108; Conserv
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The polypeptides may also be used to assay for other inhibitors of their extrative and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA AAH55098 represent oligonucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.
                                                                                           1378
                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                           gttcgcaccaaggctgaggatggttccaatgtggatatcttgatgcacattggtttcgac
                                                                                         gcaggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggta
                                                                                                                        gcaggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggta

    S. epidermidis genomic polynucleotide sequence SEQ ID NO:3464.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
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                                                                                                                                                                                                                                                                                        acaccataagttgaaaccttgagtgttcg 1527
                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                    AAH54100 standard; DNA; 2913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTD.
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sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
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                                                                                                                                                         Length 2913;
                                                                                                                                                                                               19;
                                                                                                                                                       Score 190.6; DB 22; Length
Pred. No. 2.7e-46;
0; Mismatches 364; Indels
                                                                                               Sequence 2913 BP; 1072 A; 480 C; 419 G; 942 T; 0 other;
                                                         no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                       12.5%;
55.0%;
                                                                                                                                                                           Best_Local Similarity 55.0
Matches 468; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AMAX1293 to AAX1391 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1850 ttccttattatggcacctgttaccttcttagctattggtcctatcgggacggtcatcggc 1909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                               New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctcttcggtctggtctactcaccaatcgtcatcactggtctgcaccagtccttcccgcca
                                                                                                                        Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 151.2; DB 20;
48.5%; Pred. No. 2.2e-34;
Live 0; Mismatches 533;
                                                                                                 contig SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 389-392; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                  CA;
                          BP.
                                                                                                                                                                                                                                                                                                                                  Kunsch
                         AAX12968 standard; DNA; 5840
                                                                                                faecalis genome
                                                                                                                                                                                                                                                                                                         HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                          97US-0066009.
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                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                 Dillon PJ,
                                                                                                                                                            Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-045171/04.
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                                                                                                 Enterococcus
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16-MAY-1997;
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No:1 to 391 (AAV52134 to AAV52524) recorded on it. or a representative fragment or a sequence at least 95% identical to SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No:1 to 391. AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an cisolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the cucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening of the sequences in SEQ ID NO:1 to 391, identifying members of the 10 paramy which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating man, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification or prime the amplification and isolating the amplified sequences. The computer companies are presented by the computer passed system for identifying the contains and solating the amplified sequences. The computer contains are presented by the sequence is a presented system for identifying the contains and isolating the amplified sequences. The computer passed system for identifying the contains and appropriate and sequences are computer passed system for identifying the contains and contains and computer passed system for identifying and contains and contains and contains and computer passed system for identifying and contains and contains and computer passed system for identifying and contains and contains and computer passed system for identifying and contains and contains and computer passed system for identifying and contains and contains and contains and computer passed system of the sequences.
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S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical compositions and vaccines for S. pneumoniae.
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Rosen CA;
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   DB 19; Length 3895;
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                                      619;
8.3%; Score 126.6; DB 1
llarity 47.1%; Pred. No. 3.9e-27;
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                                                                                                                                                                                                                                                                                                                                                                  The nucleotide sequence of a 3615 bp probe obtained by digestion of Escherichia coli genomic DNA with the restriction enzyme HindIII. The probes (AAQ55133-48 and AAQ55752-58) represent other probes derived, by HindIII digestion of the genomes of Staphylococcus aureus. S. epidermis, Enterococcus faecalis, Pseudomonas aeruginosa, E.coli, Klebsiella pneumoniae or Enterobacter cloacae. The probes can be used to detect their respective microorganisms in clinical samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2495 TCACACCATIGCTATGTCTGATGGTTATCACCCGTCACCTTTCTGCTGGTGGGGCCGC 2436
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                                                                           Probe; S.aureus; S.epidermis; E.faecalis; P.aeruginosa; E.coli; K.pneumoniae; E.cloacae; clinical sample; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                     infectious disease -
HindIII cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB 15; Length 3 Pred. No. 1.3e-21; 0; Mismatches 590; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3615 BP; 966 A; 962 C; 805 G; 882 T; 0 other;
                                                                                                                                                                                                                                                           Ξ,
                                                                                                                                                                                                                                                                                                    consists of a DNA fragment obtained by pathogenic bacterial genomic DNA
                                                                                                                                                                                                                                                           Uehara
                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 62-64; 100pp; Japanese.
                                                       coli genomic probe EC-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 7.18;
Similarity 46.28;
                                                                                                                                                                              93WO-JP00936
                                                                                                                                                                                                    92JP-0179719
                                                                                                                                                                                                                           PHARM IND LTD.
                                                                                                                                                                                                                                                           Ohno
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  539; Conservative
                                                                                                                                                                                                                                                                                                   Probe for identifying
                                                                                                                                                                                                                                                           Matsuhisa A,
                                                                                                                                                                                                                                                                               WPI; 1994-035086/04
                                                                                                            Escherichia coli
                                                                                                                                                                                                                        (FUSO ) FUSO
(OHNO/) OHNO
                                                                                                                                                                              07-JUL-1993;
                                                                                                                                                                                                   37-JUL-1992;
                                25-SEP-1995
                                                       Scherichia
                                                                                                                                  WO9401583-A
                                                                                                                                                        20-JAN-1994
           AAQ55752;
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Best Local S
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gtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttg
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vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genome fragment SEQ ID NO:30.
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)

Crecorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the insulant which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification or prime the amplification and isolating the amplification and solating the amplification and be used in a computer based system for identifying fragments of the S. pneumoniae genome of commercial importance, or the fragments of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneumoniae genome of commercial importance, or managements of the S. pneum
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                                                                                                                                                                                                                                                                                                                                                                                                Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
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                                                                                                                                                                                                                                                    Fannon
                                                                                                                                                                                                                                                 Dougherty BA,
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                                                                                                                                                                                                                                              Dillon PJ,
                                                          97WO-US19588
                                                                                                                     96US-0029960
                                                                                                                                                                                                                                              Cho1 GH,
Rosen CA;
                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                         WPI; 1998-272225/24
                                                          30-OCT-1997;
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CA,
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Kunsch
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and

361 421 Gaps 8979 GACCTCTTGGTAACACCATTCGTGACACTTTTGGTCATGTCTATCCTTGGACTCTTTGTC 362 attggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacagggactttat 8859 AGCATGCCATTTGGTCTTGGTGGTTTCTTGATTGGTGGGGGTTCACCAATTGATCGTCGTG 482 actggtctgcaccagtccttcccgccaattgagctggagctgtttaaccaggg---tgga AACCCATTCAACGCTATCATCACAGCTGCTATGACAGCTCAAGGTGCTGCTACTGTTGC gacttcctgatcactccagtgctgacgttgctgctcaccggattccttacattcatcgcc 8919 ATTGGACCAGTTTTCCACGTTGTTGAAAACTACATCCTTATTGCTACAAAGCGATTCTT tccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgtttggca 36; DB 19; Length 9769; 0; Mismatches 597; Indels 7.1%; Score 107.8; DB 1 46.6%; Pred. No. 2.6e-21; Best Local Similarity 46.6 Matches 552; Conservative Query Match 302 539 8739 ö g ò g ò g ð g ò

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                 ccagtgcctgcaggaacgaccaaagccgaagcagaagcacccgcagaatttcaaacgat
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getgitettggtattacggageetgegatetteggtgigaacettegeetgggeeg
                                                                      ttottcatcggtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatc
                                                                                                       TTCTTCCTTTCATTGATTGCTGGTGCAATCGGTGGTGGATTGGCTTCTATCCTTGGACTT
                                                                                                                                           779 aaggcagttgcgttgggcgctgcaggtttcttgggtgtttctattgatgctccagat
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Partial P. rubrum scrA gene region. ВР AAT47502 standard; DNA; 465 (first entry) AAT47502; 

scr operon; scrA; sucrose metabolising enzyme; sucrose isomerase; reduced metabolism; non-cariogenic sugar; trehalulose; palatinose; decomposition; monosaccharide; improved yield; disaccharide; ds.

Protaminobacter rubrum.

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misc_feature
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             16-MAR-1999
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                                                                                                                                                                                                          The present sequence comprises a partial DNA sequence from the scr operon containing the scrA gene region. The scr operon encodes sucrose metabolising enzymes, in particular sucrose isomerase. Cells containing at least one DNA sequence encoding a protein with sucrose isomerase activity, and having reduced ability to metabolise sucrose, or their extracts, optionally in an immobilised form, are used to produce non-cariogenic sugars, especially trehalulose and/or palatinose. During production of the non-cariogenic sugars, decomposition of sucrose to monosaccharides (which are difficult to separate from the product) is minimised, so the yield of the disaccharides is improved.
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                                                                                                                                                              non-cariogenic sugars, esp.
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                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 97.8; DB 18; Length 465; 53.5%; Pred. No. 4.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                         SUEDZUCKER AG MANNHEIM/OCHSENFURT
                                                                                                                                                  Cell with reduced sucrose metabolism activity - providing high yields of n trehalulose and palatinose
                                                                                                                                                                                         Claim 4; Pages 12-13; 26pp; German.
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                                                                                                                                API; 1997-054676/06
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                                                 27-JUN-1996;
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hes 204;
          EP751218-A2
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                                                                                                                                                                                                                                                                            Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                             Staphylococcus aureus contig SEQ ID #56.
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1741..1800
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CO-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained spainst S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                        /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" 25141..25200
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"...27000
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23341..23400
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
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in the production of
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stored on computer readable medium and used
anti-S.aureus vaccines
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                                  "these bases
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyellitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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                                                                                                                                                                            153 tggctgcggggggaaatgccaatgtggtccctgtttggtttagatgttgcccaagccggtt 212
                                                                                                                                                                                                                                                                                                          273 tectgeacaagegaeteaagggeaetgeagaetteetgateaeteeagtgetgaegttge 332
                                                                                                                                                Gaps
(and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                             11893 tggttaaagaagaagacttggcattaacatcttgtatttctggtatgtaggtgttactg
                                                                                                                                                                                                                                                                                                                                                                                             678 agcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcggta
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                                                                                                                                                15;
                                                                                                                Length 30246;
                                                             Sequence 30246 BP; 9663 A; 4436 C; 6386 G; 8791 T; 970 other;
                                                                                                                                              Indels
                                                                                                                DB 18;
                                                                                                                                              0; Mismatches 313;
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                                                                                                              Score 86.2; DB 18 Pred. No. 1.3e-14;
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                                                                                                              / Match 5.6%;
Local Similarity 48.5%;
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                                 computer readable medium.
                                                                                                                                                Conservative
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                                                                                                                                                Matches 309;
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Enterococcal infection;

Interococcus faecalis genome contig SEQ ID NO:639.

(first entry)

19-MAR-1999

BP.

AAX13576 standard; DNA; 474

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AAX13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The colypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can demonstance the sequences of the syndrome of the sequences can be used for the infertions of the polypeptides. The new DNA sequences can be used their fragments) are useful as primers or probes for isolating homologues of any of the Saureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents one of 5191 Staphylococcus aureus DNA sequences
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in the production of
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                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                97EP-0100117.
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                                                                                                                                                            07-JAN-1997;
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EP786519-A2
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    Score 76.4; DB 18; Length 465;
Pred. No. 1.2e-12;
0; Mismatches 146; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                   Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
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50.7%; Pred. No. 5.3e-12
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Best Local Similarity 50.7<sup>3</sup>
Matches 178; Conservative
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16-MAY-1997;
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                                    ctttatgatttcggtggtccagtcggcggtctgctcttcggtctggtctactcaccaatc 475
                                                        scr operon; scrA; sucrose metabolising enzyme; sucrose isomerase; reduced metabolism; non-cariogenic sugar; trehalulose; palatinose; decomposition; monosaccharide; improved yield; disaccharide; ds.
227 acagttattggtcccacaatgttattactatctaatggaatcacagatgctattgtttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell with reduced sucrose metabolism but with sucrose isomerase activity - providing high yields of non-cariogenic sugars, esp.
                                                                                                      gtcatcactggtctgcaccagtccttcccgccaattgagctggagctgttt 526
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                                                                                                                                                                                                                                                                                                                                    Partial Enterobacter sp. scrA gene region.
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4.7%; Score 71.6; DB 18; Length 357; llarity 53.1%; Pred. No. 2.7e-11; Conservative 0; Mismatches 134; Indels 0.

Query Match Best Local Similarity Matches 152; Conserv

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Sequence

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Description

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Copyright (c) 1993 - 2000 Compugen Ltd.
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ERWBGPA BSU34876 BACISPQ STSCRCOMP BACSACP BSGENR BSUB0020

STSCRA AE007479 SPNEU1902 AF206272

AX144742 AP001514 AF229829 AP001513 AP001508 KPSCRYAB EAM250722

SXSCRA BSTREAPR D83967

D86417 BSUB0005

PPSURFOP LLZ97015 AE004395 STRSCRA AE006222 VIBSCRAK

Corynebacterium.

(Corynebacterium.

(Corynebacterium.

(Dases 1 to 1527)

Pompejus. M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G.

Orynebacterium glutamicum genes encoding phosphoenolpyruyat e:
sugar phosphotransferase system proteins
Patent: WO 0102883-A 1 11-3AN-2001;

BASF AKTIENGESELLSCHAFT (DE)

Location/Qualifiers

1. 1527 25-JAN-2001 Corynebacterium glutamicum. Corynebacterium glutamicum Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; PAT AX069134 1527 bp DNA Sequence 1 from Patent W00102583. AX069134 GI:12579016 source AUTHORS TITLE JOURNAL FEATURES

SUMMARIES

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ALIGNMENTS

AE000449 AP001509 AR012068

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Ozaki,A.
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Corynebacterium.
1 (bases 1 to 349980)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M.
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and
Novel polynucleotides
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Bacteria; Firmicutes; Actinobacteria;
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Yokoi,phrucleotides
Patent: EP 1108790-A 2904 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
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re 1492; DB 6; Length 1983; d. No. 0; Mismatches 0; Indels 1; Gaps	ctcatggcatctgcgccgttcgcgttcttgccagtgttggttg	cgtttcggcggcaatgagttcctgggcgccgcgtattggtatggcatggtgttcccgag 120 	cttggtgaacggctacgacgtggccgccaccatggctgcgggcgaaatgccaatgtggtc 180 	cctgtttggtttagatgttgcccaagccggttaccagggcaccgtgcttcctgtgctggt 240 	ggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgc 300 	agacttcctgatcactccagtgctgacgttgctgctcaccggattccttacattcatcgc 360	cattggcccagcatgcgctggtggggatgtgctggcacacggtctacagggacttta 420	tgatttcggtggtccagtcgggtctgctcttcggtctggtctactcaccaatcgtcat 480	cactggtctgcaccagtccttcccgccaattgagctggagctgtttaaccagggtggatc 540 	cttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgtttggcagt 600	gttetteetggggaagaggaaaageteaagggeettgeaggtgetteaggtgteteege 660 	tgttcttggtattacggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgtt 720	<pre>cttcatcggtatcggtatcggcagctatcggtggcgctttgattgcactctttaatatcaa 780 !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! CTTCATCGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTAATATCAA 125</pre>	ggcagttgcgttgggcgctgcaggtttcttgggtgttgtttctattgatgctccagatat 840 	ggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgcagcgattgc 900 	ttatggcctttacttggttcgccgcaacggcaqcattgatccaqatgcaaccgctgctcc 960 	agaagcaccgcagaatttcaaacgattc 1020 
97.7%; Scc imilarity 99.9%; Pre ; Conservative 0;	1 ctcatggcatctgcgccgttcgcgttcttg 														ggtcatgttcttggtgtgtgtgcagttgttac 	ttatggcctttacttggttcgccgcaacgg 	agtgoctgcaggaacgaacgaagcgaagcagaagcaccgcagaatttcaaacgattc 
Query Match Best Local S Matches 1503	Oy 1 Db 481	Qy 61 Db 541	Oy 121 Db 600	Qy 181 Db 660	Qy 241 Db 720	Qy 301 Db 780	Qy 361 Db 840	Qy 421 Db 900	Qy 481 Db 960	Oy 541 Db 1020	Qy 601 Db 1080	Oy 661 Db 1140	Oy 721 Db 1200	Oy 781 Db 1260	Qy 841 Db 1320	Qy 901 Db 1380	Qy 961 Db 1440

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1021	1081	1141	1201	1261	1321	1381	1441	1501	T 4 136 ITION SION ON	U)	REFERENCE AUTHORS TITLE	JOURNAL FEATURES	SOULC	
Qy Dp	Qy	Qy	Oy Dp	Qy	Qy Db	QY	QY Db	ΟŊ	RESUL AX069 LOCUS DEFIN ACCES VERSI	SOURCE	REF.	FEAT		

ORIGI			
W B C	Query Match72.5%;Score 1107.4;DB 6;Length 1109;Best Local Similarity99.9%;Pred. No. 3.7e-289;Matches 1108;Conservative0;Mismatches1;Indels0;	Qy 1439 ggcgaaat            Db 1021 GGCGAAAT	1439 ggcgaaattgaagcgggagccaacctgctcaacgtcgcaaagaaag
Qy Db	tatgatttcggtggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtc 478	Oy 1499 acaccata             Db 1081 ACACCATA	1499 acaccataagttgaaaccttgagtgttcg 1527 
Oy Op	479 atcactggtctgcaccagtccttcccgccaattgagctggagctgtttaaccagggtgga 538 	Ĺ	PER 21838 bp DNA BCT 23-MAY-1994
Qy Db	539 tccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgtttggca 598	DEFINITION PEROLOCOCCU ACCESSION L32093 VERSION L32093.1 KEYWORDS agaR gene;	is pencosaceus railinose operon genes. GI:493181 agaS gene; agl gene; alpha-galactosidase;
oy B	599 gtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcaggtgtctcc 658 		alpha-glucosidase; fructokinase; insertion element; permease; raip gene; rafk gene; raffinose operon; regulatory protein; scrA gene; scrB gene; scrK gene; scrR gene; sucrase; sucrose-6-phosphate; transport protein.
oy ob	659 gctgttcttggtattacggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccg 718 	SOURCE Pedioc IS30 h Kingdo DNA; I	occus pentosaceus (strain PPEL.U) UNA; insertion sequence pamolog (transposable element insertion sequence IS30 homolog, n Prokaryotae) DNA; Pediococcus pentosaceus (strain PPEL.U) nsertion sequence IS3 homolog (transposable element Insertion
oy Dp	719 ttetteateggtateggtacegeageteggggegetttgattgeactettaatate 778 	sequen pentos ORGANISM Pedioc	sequence IS3 homolog, Kingdom Prokaryotae) DNA; and Pediococcus pentosaccus (strain PPE1.0) DNA. Pediococcus pentosaccus Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Oy Op	779 aaggcagttgcgttgggcgctgcaggtttcttgggtgttgttctattgatgctccagat 838 		Pediococcus. 1 (bases 1 to 21838) Leenhouts,K.J., Bolhuis,A.A., Kok,J.J. and Venema,G.G. The sucrose and raffinose operons of Pediococcus pentosaceus PPB1.0
Oy Dp	839 atggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgcagcgatt 898 	JOURNAL UNDUBL. COMMENT ON MAY FEATURES SOURCE	1896 25, 1994 this sequence version replaced gi:475106. Location/Qualifiers 1. 21838
oy op	899 gcttatggcctttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgct 958 	repeat_unit	/organism="Pediococcus pentosaceus" /strain="PE1:0" /db_xref="taxon:1255" /487. 510
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Οy	accacgccgattgttttcgaattacaagaaaaccggacctgtaaacacttacggtttg 	-10_signal -35_signal	<pre>complement(38373842) /gene="rafR" complement(38593864)</pre>

gene

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AMASAPFTFLPILLGFSATKRFGGNPYLGATMGMINVLPSLVNGYSVATTMAAGKMYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFEPMPSGSHAFANDPTERFPYSVTSLPLEYSTIGSGDYRQPAYVIKDANNQLLPILE
YTGFSVNDQPINSRQLPPTVSKHTPVTTLVIHLTDAVTKLQMDLNYTIFENQPLILRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVNLNGEHFTTNVOKGDTVHQGDLLGTFDIAALKAANYDPTVMLIVTNTANYANVERL
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5976. 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGNKALDNRMYSLVTLI IMVLRI VELFIDPFIGNAIDRTKNSPGHFRPWVVGGTVSS
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Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
Unpublished
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     Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                Direct Submission
Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological
Sciences, Department of Genetics, Kerklaan 30, Haren, The
Netherlands, 9751 NN
On May 26, 1994 this sequence version replaced g1:475962.
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244 ttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgcaga 303 15085 cGcCTTCATTCTTGCTTGAAAATTCTTCCATAAACACATTAAAGGGGCATTTGA 15026
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P.pentosaceus (PPE1.0) sucrose and raffinose operons
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58.8%;
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LNHLRLSWSPGRITSYTELSTROPYQABLAOTALISTRIALIFUEL
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PGDDFKSCHOFYHDICLEGLAAGPAVGKRTGKRGKDIPVDDPVWPIITDYIAQACVNLT
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GLLLAQAALKNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="enzyme II of the PTS system, sucrose specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15324 ATGGCTAGTGCGCCGTTTACTTTCTTGCCAATCCTCTTAGGATTTTCAGCAACGAAGCGC 15265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15205 AGTTAACGGCTATAGCGTTGCAACGACCATGGCAGCCGGCAAGATGGTTTACTGGAACGT 151.46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgcaga 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 cttcctgatcactccagtgctgacgttgctgctcaccggattccttacattcatcgccat 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ggtgaacggctacgacgtggccgccaccatggctgcgggcgaaatgccaatgtggtccct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21839;
                                                                                                                                                                                                                 /function="fructose 6-phosphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 287.6; DB 1;
Pred. No. 8e-67;
0; Mismatches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ilscr"
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                                                                                                                        .11593)
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enzyme II sucrose protein; fructokinase; sacA gene; sacB gene; sacK
gene; sacR gene; sucrose-6-phosphate hydrolase.
Lactococcus lactis.
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Luesink, E.J., Marugg, J.D., Kuipers, O.P. and de Vos, W.M.
Characterization of the divergent sacBK and sacAR operons, involved
In sucrose utilization by Lactococcus lactis
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Lactococcus.
                                                                                                                                                                                                               15025 CTTCACGTTTACCCCGATGTTTGCCATTGTGATTACTGGTTTCCTAACTTTTACAATCGT 14966
                                                                                                                               14785 TGGTGGTTCCTTTATCTTCCAGTCGCCTCGATGGCCAACATTGGGCAAGGTGCCGCCAC 14726
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Location/Qualifiers
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LL297015 5800 bp DNA BCT
Lactococcus lactis cremoris sucrose gene cluster.
297015
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/sub_species="cremoris"
/db_xref="taxon:1358"
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Luesink, E.J.
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                                                                                                        1905 TGGTATTGGTGGAGACTTTATTTTTCCAGTTGCGGCCTGCGCAAATATGGCTCAAGCTGG
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//brotein_id="CAB09691.1"
//brotein_id="CAB09691.1"
//translation="Wavyvos!rapagetheviakekfrattpoetiskt
IKYFKENRVSAIGLGSFGPIDLALSSKTYGYITSTPKVGMRNINLVGGLKEALDIPTY
IKYFKENRVSAIGLGSFGPIDLALSSKTYGYITSTPKVGMRNINLVGGLKEALDIPTY
IKYFKENRVSAIGLGSFGPIDLALGSFGTGGGGATGONGYFGTGGGGGGGGGGRANGHRIN
DVLTPFGGIGPFHGDGLEGVAAGPSLEARTGILGERISSDPINDLISYYIAQAAINAT
LTLAPECIILGGGVMEKPNMISLIOKOFISMLNNYIDLPCSVEKYIRLPTVKENGSAT
                                                                                                                                     TFTIVGPALRFVSNGLTDGLVGLYNTLGALGMLVFGGFYSAITVTGLHGDSFPALETML
THYOHGGIGGDFIPPAACANMAQGATFALLEVTKNIKTKALAAPAGVSALLGITE
PALEGINLKKYPFFALGASAITGSLEMGLFHVLAVSLGSAGLIGFTE
ISTFISFLIAFVVTSIYGRRMEAKSITKEKNKONATTOYOPEKVIIDPVKSGELLAPI
NGVIPLSDSVSDPVFSKEINGKGIAHKPKSGELFSPAGGEIIIAYETGHAYOIKTKNG
GEVLLHIGIDTVSMGNGFIONVKOGKVKAGDLLGSFDKEEIKKSGLDDTVIIVTN
SASYNEILPLSENVDIKVGEXILLLN
                                                                                     VMALVKLLSDIFVPLIPALVAGGLIMALNNALTAEHLFATKSLVEMFPMWKGFADIVN
TMSAAPFTFWPILIGYSATKRFGGNPYLGAVVGMIMVMPGLINGYNVAEAISNHTMTY
WDIFGFKVAQAGYQGQVLPVIGVAFILAKLERFFHKYLNDAIDFTFTPLLSVIITGFL
                                                  /translation-"MNHKQVAERILNAVGRDNIQGARHCATRLRLVLKDTGVIDQEAL
DNDPDLKGTFEAAGGYQIIVGPGDVNTVYEEFIKLTGISEASTADLKEIAGSQKKQNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGGCCGAAATCCATATTTAGGTGCTG-TTGTAGGTATGATTATGGTGATGCCTGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTTTTATCCTTGCTAAACTTGAGAGATTCTTTCATAAATACCTTAACGATGCTATAGA
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protein"
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Pred. No. 7.2e-57;
0; Mismatches 647;
/product="enzyme II sucrose
/protein_id="CAB09690.1"
/db_xref="GI:4581477"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996
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                                                                                                                                                                                                                                                                                                                                                                          number-"2.7.1.4"
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                                                                                                                                                                                                                                                                                        ..38. .5720
/gene="sack"
4848. .5720
/gene="sack"
/EC_numb-
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                                                                                                                                                                                                                                                                4838. .4842
/gene="sack"
4838. .5720
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51.1%;
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Best Local S:
Matches 725,
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ORIGIN
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                 Bacteria: Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. 1 (bases 1 to 10264)
Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Oin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg, J. F. Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Sellers, P., Willer, W. Wanathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Direct Submission Pereser, C.M.

Submitted (14-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MOYPVIAKQLLESLGGKSNIQALAHCATRLRLVLNDETQINESA
IESLQGVKGGFKVAGOYQIIFGSGIVNQVYAEMAKLTGLVEMSTNDVASAGAEKQNWA
GRAVKGLEDIPYRIIPAIVAGGLLGMGLFNVLTAPBGLFIEGQSLIDANFOCLADLASMIN
TFAARPFVYLDVLLAFSASKRFGGNFLGAALGMLWHPDLLNGWGFGSASVGGTYN
WNILGFEIEKVGYQGSVLPVLVSAYILAKIENGLRKIVPSVVONLLTPMLAIFTGFL
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LADIVTTGGTFIFPTAAMSNIAQGAAALAVGVMTKETKLKGVA1PSGVTALLGTTEPA
MFGVNLKLRYPFTAAICGAALASAFTTLFNVKAQALGAAGLAGIISINPQQIGYYIMG
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KEIEYIQIFNQKRVEGIVFYATHLDQPLVHAIQHSAVPVVLVGQDGSLYNIPSIVHDD
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SIESGYQMAKQAYLDYPQLDGLFCATDRLAVGAIKALGELGVHVGQQVKLLGVGNDEL
AYVSNPPLSTFNYAFDKAGENAAKMLLERIAGRGQEMSKVVLTFQNIQRETCPV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="PTS system, sucrose-specific IIBC component"
/protein_id="AAF96554.1"
/db_xref="GI:9658069"
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/protein_id="AAF96555.1"
/db_xref="GI:9658070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:M76768 SP:P22825 PID:155262;
identified by sequence similarity; putative"
/codon_start=1
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    10264
    organism="Vibrio cholerae"

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/gene="VCA0653"
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2922. .456°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="N16961"
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/gene="VCA0654"
1854. .2846
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/gene="VCA0654"
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ORGANISM
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JOURNAL
                                                                                   AUTHORS
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                                                        REFERENCE
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Gapanvavalarlcssafegrygnoppgremogotipdegvdcqhiredpyhtrstvv
vdldehgersftfmvkpsadqflqlsdipspongemlhvcsialanqpsrsstfaala
OMKEVGGYVSppDnlrREVWSPPQELQATVMRAVGLADVVKFSEEELQFLTGTQSIEE
GLQAIADFQIPLVVTLGAKGALVYTPNSRQIVSGRAVKPIDTTGAGDAFVRGL
SVAQDHHNQATLIDAVKWANGCGALATTQKGAMTALPNQAALXAFLE"
6008. 7546
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TKSGGFYWVDAYVTDIYQQGQLTGYQSVRVKAERKWVEIATKAYQALLAAEKAGKKIQ
FKLHTSLRYALLLGALMSPALAHGFQAPEQWQWIASLLPAGVLGLLFRQELVRTPQQL
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WYGPLNBRAHYSSPYGIRLIQGSHITYPRIHDEPQAYILDUBDKRIVEYIPYLDDYS
MIGTTDVEYKGDPRKYAITDAERDYLISIVKHFMRETARSDIJAEFSGYRPLCDDES
NSPQAITRDYILSLDQQADEAPLLSIFGGKLTTYRKLGEAAMKHLAPFFPKMKAPWTA
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/db_xref="G1:9658074"
/translation="MYTFALIKITLEQQAEMSAYTPSAQQEVLVGDHDQLVSTTDLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQWQNEYDSISRLIYSGADAFSVADYHLKMASARIRTILGRMMDSARPLGELANQLHL
TTQEYHQALAAQNSNIQAVTQATDÄVESAAERVSSHTHSAHQLIDQVQDHCAETKHSI
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KDFASATSSASSKLVHGGLRYLEHYEFRLVSEALAEREVLLKKAPHIVTPMRFRLPHR
PFLRPAWMIRAGLFLYDNLGKRTSLPASHKVNLKAGSVTKPEWQIGFEYSDCWVDDAR
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FSGELYQREIDYLCEKEFARHAQDIFWRRSKLGLNHDTSVVEEVESYLQQKFHAEQPL
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// Appne="VCA0657"

// Appne="NCA0657"

// Appne="Similar to SP:P13035 GB:M21277 GB:M55989 GB:M96795

PID:146181; identified by sequence similarity; putative"

// Codon_start=1
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/protein_id="AAF96558.1"
/db_xref="GI:9658073"
β
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/note="similar to GB:M74035 PID:155269; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:M76768 SP:P22824 PID:155263;
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                                                                                                                                                                                                /product="sucrose-6-phosphate dehydrogenase"
/protein_id="AAF96556.1"
/db_xref="GI:9658071"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified by sequence similarity; putative"
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                                           sequence similarity; putative
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/protein_id="AAF96557.1"
/db_xref="G1:9658072"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4690. .5661)
/gene="VCA0656"
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NVTHONLQRLATQAESAALTTLKLSDQAQQVQQLMTEIGGIAEQTNLLALNAAIEAAR
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complement(10068..10190)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 GTTTGGCGGTAACCCCTTTTTGGCCGCTGCG-CTGGGTATGCTGATGGTGCATCCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAACTTGCTTACCCCAATGCTGGCGATTTTTATCACGGGTTTTCTGACCTTTACTGTGG
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Pred. No. 1e-51;
0; Mismatches 387; Indels
                                                                                                                                                                                                                                                                                                                                                                             /gene="VCA0660"
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                                                                                                                                                                                                           /product="protein F-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
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55.4%;
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VIITGFLTFIVIGPVWKEVSDWLTNGIVWLYDTTGFLGMGVFGALYSPVVMTGLHQSF
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by H.K.Karamitsu, 22-FEB-1989.
Location/Qualiflers
1. .2508
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                                                                                                                                                                                413
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Sato, Y., Poy, F., Jacobson, G.R. and Kuramitsu, H.K.
Characterization and sequence analysis of the scrA gene encod
enzyme Ilscr of the Streptococcus mutans phosphoenolpyruvate-
dependent sucrose phosphotransferase system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       887
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CTTTAGCTGTGGGTGTGATGACGAAAGAGACCCAAACTCAAAGGGGTCGCGATTCCTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                           getggeegttettcateggtateggtacegeagetateggtggegetttgattgeaetet
                                                                                                           gtttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme scr-II; phosphoenolpyruvate-dependent sucrose phosphotransferase system; sucrose-6-phosphate hydrolase
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ALGITEPALFGVNLKYRFPFFCALIGSASAAAIAGLLQVVAVSLGSAGFLGFLSIKA
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-MAR-2001 Pathobiology St. Paul, MN Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Pasteurella. and Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 08-the Submitted (24-OCT-2000) Department of Veterinary University of Minnesota, 1971 Commonwealth Ave., 55108, USA οţ 204 BCT of Paustian, M.L., section 189 1 (bases 1 to 10085) May, B.J., Zhang, Q., Li, L.L., DNA PM70 8 GI:12722266 Pasteurella multocida. Pasteurella multocida AE006222 10085 bp Pasteurella multocida 2 (bases 1 to 10085) Zhang, Q. and Kapur, V. Direct Submission AE006222 AE004439 AE006222.1 Kapur, V. 21145866 genome AE006222/c LOCUS ORGANISM ACCESSION TITLE JOURNAL TITLE VERSION KEYWORDS REFERENCE AUTHORS AUTHORS MEDLINE REFERENCE SOURCE

Location/Qualifiers

FEATURES

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54.5%;
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Best Local Similarity
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Vibrio alginolyticus
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 2955)
Blatch,G.L., Scholle,R.R. and Woods,D.R.
Nucleotide sequence and analysis of the Vibrio alginolyticus
Gencose uptake-encoding region
Gene 95, 17-23 (1990)
91071601
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                                                                                                                 ttcggtggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtcatcact
                                                                                                                                                                         ggtctgcaccagtccttcccgccaattgagctggagctgttt------aaccag
                                                                                                                                                                                                   1356 GGTATGCATCACAGCTTCATTGCGATTGAAACTCCAACTTCTTGCGGATATTGCAACGACG
                                                                                                                                                                                                                                                           1416 GGGGCACCTTTATCTTTCCTATTGCGGCGATGTCTAACGTTTCTCAAGGAGCGGCAGCG
                                                                                                                                                                                                                                                                                         ttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcaggt
                                                                                                                                                                                                                                                                                                                                                gtctccgctgttcttggtattacggagcctgcgatcttcggtgtgaaccttcgcctgcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                  1596 TACCCATTTATTGCGGCAGTTTGCGCTGCGGCGTTATCAAGTGCGTTCATCAAGTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatatcaaggcagttgcgttgggcgctgcaggtttcttggggtgttgttctattgatgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccagatatggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane protein; scrA gene; sucrose transport protein.
Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXSCRA 2655 bp DNA BCT
S.xylosus scrA gene and unidentified open reading
X69800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus xylosus
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
1 (bases 1 to 2655)
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1. .2655
/organism="Staphylococcus xylosus"
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Mol. Gen. Genet. 241 (1-2), 33-41
94049686
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Direct Submission
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TITLE
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//CTATESTATION—"MNYKRARNILQALGGEDNVEAWTHCATRIRLVLKDEGLVDERA

CAGDNOVWCRFSTGGOYQVIIGSGTVNKVESELEKITGKERSSYSEWYTGGTKNMNPF

ORFUKALSDIEVPI ITAAIVAGGLAMGINNILTAAPGIEVDNOSLIEVONOFSGLAEMIN

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LIADSSSTGGSFIFTATMSNNAOGAAALAAFFIIKRNKKLKGVASAAGVSALGITE

YGIAMITAFIVAFGYTYALSSTYAFFKVKRINEA"

347 C 976
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/db_xref="Sptre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1656 ATGAGTGCTTATGATTATCCTAAAGCATTAGAAGCGGGAAAAGAGATTCCTCATTGGAAC 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        teggeggeaatgagtteetgggegeegetattggtatggegatggtgtteeegagettg 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 gigaacggciacgacgiggccgccaccaiggcigcgggcgaa---aigccaaigiggicc 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 5.6e-46;
); Mismatches 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(132. .137)
                                        /db_xref="taxon:1288'
                                                                                                                                                                                                              complement(<1. .121)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/transl_table=11
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                                                                                                                                                                      /clone="pSE4"
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56.2%;
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1053. .2495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF2"
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Best Local Similarity
Matches 485; Conserv
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-10_signal
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AIVLIVPFAGTYAYGRFKHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tre, domains B and C" corresponds to position 1 of x80203"
Submitted (27-SEP-1995) Dahl M. K., University of Erlangen-Nuernberg, Lehstuhl fuer Mikrobiologie, Staudtstr. Erlangen, Fed. Rep. of Germany, 91058 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="repressor of the trehalose operon"
/note="position 3684 corresponds to position 2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name="phosphotrehalase"
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                                                                                                                                                                             /strain="168 Marburg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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167. .1579
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3352. .4068
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167. .1579
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                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helfert,C., Gotsche,S. and Dahl,M.K.
Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed
by a phospho-alpha-(1-1)-glucosidase encoded by the treA gene
Mol. Microbiol. 16 (1), 111-120 (1995)
95379486
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Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                   2015
                                                                                                                                                                                                                                                                              1896 GTTGGTCCATTAACACGTACTTTAGGTATTGGTTATACAACGTGTGCTATAT 1955
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B.subtilis treA, treP and treR genes.
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Dahl, M.K.
Direct Submission
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IYEYIEGELGISIZYAQKEITAEPCTDEDRELLDLRGYDHWVVRNYFLEDTSLFQY
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Pred. No. 1.5e-44;
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53.1%;
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YfjR.
                                                                                                                                                                                                                                                                                                                         Bacillus/Staphylococcus group; Bacillus.
(passes 1 to 22197)
Sekjquchi, J.
Direct Submission
Submitted (08-MR-1996) to the DDBJ/EWBL/GenBank databases. Jun Sekjquchi, Textlle Science and Technology, Shinshu University, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano, Japan (E-mail:)sekiqu@giptc.shinshu-u.ac.jp, Tel:0268-21-5344,
                                                                                                                                              20-NOV-1997
                                                                                                                                                                                                                             YfkK; YfkJ;
YfjT; YfjS;
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Nucleotide sequence analysis of B. subtilis cromosome in
                                                                                                                                                                                                                                                                                                          Bacillus/Clostridium group;
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C DNA, 74 degree region
                                                                                                                                                                                                                         TreP; TreC; TreR; YfkP; YfkO; YfkN; YfkH; YfkH; YfkH; YfkB; YfkB; YfkB; YfkB; YfkB; YfkB; YfkB; YfkB; YfkB; YfkA; Bacillus subtilis (strain:AC327) DNA.
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complement(1777..1962)
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2 (bases 1 to 22197)
Sekiguchi, J., Yamamoto
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                                                                                                                                                                                   ACCESSION
VERSION
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AUTHORS
                                                                                                  RESULT 1,
D83967/c
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9418. 9435
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9741. .10931
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YISENLVHTFHSVAEQFGWSELFIGVIIVAIVGNAAEHASAIIMAFKNKMDIAVEIAV
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complement(6027. .6046)
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complement(4109. .4903)
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EENNI"
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Korladif Krbehmtaallalladarqberiydlandındagalığıdıksnasfhaarkngk
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                                                       Direct Submission
Submitted (09-JUL-1996) to the DDBJ/EMBL/GenBank databases. Junichi
Sekiguchi, Textile Science and Technology, Shinshu University,
Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386,
Japan (E-mail:jsekigu@@iptc.shinshu:u.ac.jp, Tel:0268-21-5344,
                                                                                                                                                                                                    Yamamoto, H., Uchiyama, S., Nugroho, F.A. and Sekiguchi, J. Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis, genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein 97417488
    group; Bacillus
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                                            Sekiguchi, J
                                                                                                                                                                                         2 (sites)
                     REFERENCE
AUTHORS
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Bacillus subtilis (strain:AC327) DNA.
Bacteria: Rirmicutes; Bacillus/Clostridium group;
                                                                                                                                              TTTGCTGAATGCGTGGGGATATGGCGCGCGCAGAACAAAGCGGAGAGATCCCGGTATGGAA 20206
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                                                                                                                                                                                                                                                                                                                                                                    cattggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacagggactta 420
                                                                                                                                                                                                        ggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgc 300
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PLLESLEQPFYTKFITLSNHFPFGMDEGDTDFPAGDFGDSVVDNYFQSAHYLDQSIEQ
FFDLKKGLTDGYDGTDTWFPFGMDEGDTDFPAGAVLGKDETTDVDMAGLQRVPLEIH
AAGVKGEKVHYFQTTVVDVAPFILLLLGVDTRDYLMAGSDILGSKEHREVIPFRAGDFIS
PKYTKISGKYYDTKTGKELDESEVDKSEDSLVKKELEMSDKIINGDLLRFYEPKGFKK
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FMFLSPLLYAVHAVLTGLSLFIVNWLGIRSGPSFSAGAIDYVLSYGIAEKPLLLLLVG
ICYAAVYFIVFYVLIKALNLKTPGREDDDVDEVLDENTVQDVNENIMLKGLGGKENLQ
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YSDTGISFVLGEGEERLHKLCQCAENAFQKGLQQAKAGKRQNQIGRAVYHEARSQGFT
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                                                                          KNYTSATFHGNTQTFWNRNEMYKAEGIDKFFDSAYYDMNEENTKNYGMKDKPFFKESM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIDHCATRLRLTVKDTALVDEALLKKAGAKGVVKSGGQSVQVIIGPNVEFAAEELRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MIVTNDQELEGLKKIGRIVALAREEMKRKAEPGMSTKDLDLIGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           866 TTTGCTGAATGCGTGGGGATATGGCGCGCGGAAAAAGCGGAGAGATCCCGGTATGGAA
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Pred. No. 1.5e-43;
0; Mismatches 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTFKTPDKSMVAQVEHTIVITKDEPIILTKL"
                                                                                                                                                                                                     VNPSDYDYTKHDEDSSETSKDNEDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(11176. .11195)
                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA22299.1"
/db_xref="GI:2443228"
                                                                                                                                                                                                                             complement(9789. .9820) complement(9820. .11178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAA22300.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11334. .11352
11350. .12099
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/transl_table=11
/product="Yf1G"
                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                                                                                   /product="YflF"
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Matches 482; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   TQIELQNLTPVFEGLIPYLQSGYYAFGTMGELIILPLLFSNRSVPLKYTIFAILLGAL
LLAVMLFSSISVFGPNLTSTFFDPAYMVIRQIRITDFLDRSDLIIAAFWIPVIMVKIA
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IPSIMVQGNSVSVSLAETFSFNKIYAGIGIAFLIGLVVIGGVKRIGKVTEFVVPLMAG
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EAGMGTAPIAHAAAMTDHPVRQGFWSVIGIVIDTLIICTTTAFIVLASGVWTGKNASN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGYRILKNAGMAEDEGALKKELMTIDHLIEKCYDEKEREQLIRK
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MQAKTNGGQLGDSAFSLMRPTDAFYFIDTIILLIILAIKVNKPAETSSKKSFRIIFASS
                                                                                                                                                                                                                                                                                                                                VVIVIPALWLMHRLMKKHQDKNIYELLSDSSPIAGRIIILLFSLYFLLINAHDIRFFI
NLINILFLPRTPWAVLGGVIIFVAICIAREGKETLTRWAQIFLFPFGILVLFLPFTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation = "MMDFSHIVSEDKIKRAIKDGDFQNLPGMGKPLPKMTRHTCRNRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'translation="MREKVAKNAVESTFREDITKCKTRYLSRNKGIKWYIENCMIKYK
                                                                                                                                                                                                                                                                                                           /translation-"MDKTSAYQGLFFGALYTLAVGLKHAPILMIESAKQNAWHSYILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVYLAAIIIGAAGGAKAIWGVLDLALVFIVVPNVIALLLLSRKVKALYTEFFTSEQYY
LKDIRKTKQKPVYPTKEAKNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLLLPLLIYLIIKSKALFGAKAKH" complement(5650. .7065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA22294.1"
/db_xref="GI:2443223"
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/db_xref="Gi:2443225"
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/db_xref="GI:2443227"
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complement(7582. 7596)
complement(7600. 7737)
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complement(7149. .7175)
complement(7190. .7450)
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                                                                                                                                                                                                                                                                                /db_xref="GI:2443222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
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/transl_table=11
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/product="Yfks"
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481 cactggtctgcaccagtccttcccgccaattgagctggagct----gtttaaccaggg 534
                                                                                                                                                                                                                                   775 tatcaaggcagttgcgttgggcgctgcaggtttcttgggtgttgtttctattgatgctcc 834
                                                                                                                                                                                                                                                 206 TOTGCTGGCAAGCTCCGTCGGTGTCGCCGGGGATTTTCTCATCATGAGCCA 147
                                                                                                                                                                                                                                                                      835 agatatggtcatgttcttggtgtgtgtgcattgttaccttcttcatcgcattcggcgcagc 894
626 TATCGGCCCGATTACATTTGCGATCGGTAATGTACTGACTTCAGGGCTTATCTCGGTGTT 567
                                                                                                                                                                                                                                                                                        146 GTACTGGGGCGCGTTTGCAATCGGGATGGCTATTGTATTGATCGTGCCGTTTGCCGGAAC 87
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Search completed: March 22, 2002, 08:49:30 Job time: 7679 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

- protein search, using sw model OM protein Run on:

US-09-604-231-2

1 MAMVFPSLVNGYDVAATMAA......IEAGANLLNVAKKEAVPATP 468 Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 hits satisfying chosen parameters: of Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phosphotransferase	phosphotransferase	scrA protein - Sta	PTS system, beta-g		sphotrans	PTS system, sucros	beta-glucoside per	sucrose uptake pro	hypothetical prote	beta-glucoside-spe	hypothetical prote	photrans	PTS system, trehal	phosphotransferase	phosphotransferase	PTS system, sucros	phosphotransferase	sac operon regulat	levansucrase synth	phosphotransferase	phosphotransferase	PTS system enzyme	PTS system, sucros	phosphotransferase	PTS system, trehal	phosphotransferase	phosphotransferase	, hypothetical prote
SUMMARIES	ID	S44257	B32243	839978	н83686	C83724	S68599	F82432	I40406	JQ0781	T47097	B42603	D86807	C69725	н83926	C25977	862331	H83881	WQEBST	139868	JU0293	A39938	C65236	A86122	F84096	S46953	B82263	WQBSGS	S18607	D86766
	DB .	~	<del>, -1</del>	7				7		7	7										7									
	Length	651	664	480	630	636	632	479	609	479	609	631	636	470	470	625	456	458	455	372	459	460	473	473	453	692	478	669	651	195
æ	Query	44.8	40.4	29.7	29.4	28.5	28.5	27.9	27.8	27.3	27.3	27.1	24.9	24.1	24.1	24.0	20.7	20.6	20.0	19.8	17.2	16.5	15.5	15.2	14.5	14.5	14.3	13.6	13.4	13.3
	Score	1058.5	953.5	701	695.5	673.5	673	629	657	646	645	640	588.5	570	569.5	567.5	489	487	473	467	406	390	367	360	342.5	341.5	339	321.5	317.5	314
	Result No.	7	2	Э	4	S	9	7	æ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

PTS system, glucos phosphotransferase	hypothetical prote phosphotransferase phosphotransferase	hypothetical prote sucrose phosphotra hypothetical prote	PTS system, glucos phosphotransferase hypothetical prote	phosphotransferase phosphotransferase lactose transport	probable PTS enzym hypothetical prote
D83755 WQEC2N	E85567 S46952 D69750	C86678 B69744 C86766	C83839 G65051 B85920	F70169 H69940 A32241	G85885 D65017
7	777	000	000	000	77
675 648	648 675 631	521 446 454	173 485 485	189 168 634	474
12.9 12.6	12.6 12.3 12.2	12.1 12.0 11.9	11.5 11.4 11.2	10.8 10.8 10.8	10.7
305.5 298.5	297.5 289.5 287.5	285 283.5 281	271.5 270.5 265.5	256 255 254.5	253.5 250.5
30 31	3 3 4 4	35 36 37	38 39 40	4 4 4 3 2 3	44

## ALIGNMENTS



Cyaccession: S44257
Riceahouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Riceahouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Riceahouts, T.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Riceahouts, T.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
Rybescription: The sucrose and raffinose operons of Pediococcus pentosaceus PPEL.O.
A; Reference number: S44257
A; Molecule type: DNA
A; Residues: 1-631 < LEE>
A; Coss-references: EMBL: 232771; NID: 493728; PIDN: CAA@3668.1; PID: 9475968
C; Genetics: Ccrast-references: EMBL: 232771; NID: 493728; PIDN: CAA@3668.1; PID: 9475968
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C; Genetics: Ccrast-references: EMBL: 232771; NID: 9493728; PIDN: CAA@3668.1; PID: 9475968
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C; Genetics: Ccrast-references: EMBL: 232771; NID: 9493728; PIDN: CAA@3668.1; PID: 9475968
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ŝ Gaps 23; Length 651; 78; Mismatches 151; Indels DB 2; 44.8%; Score 1058.5; DB 46.7%; Pred. No. 1.4e-65; Matches 221; Conservative Best Local Similarity Query Match

1 MAMYFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60 g ŏ

61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120 ŏ g

121 VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176 δy

g

177 KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF

ò

236

qq

486 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 237 δ qq

356 AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV ŏ

487

g

357 VAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI ò

596 q

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R;Wagner, E.; Goetz, F.; Brueckner, R.
Mol. Gen. Genet. 241, 33-41, 1993
A;Title: Cloning and characterization of t
A;Reference number: S39976; MUID:94049686
A;Accession: S39978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 108;
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Matches 152; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    374 YFLTKDKKKKGLSSSSGVSALLGITEPALFGVNLKYRPPFFCALIGSASAAAIAGLLQVV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 VPAGTTKAEAEAPAEFSNDST-----IIQAPLTGEAIALSSVSDAMFASGKLGSGVAI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY-GLGEIEAGANLLNVA 459
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                              FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
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                                       649
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                              DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL - - LNVAKKEAVPAT
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                        Query Match 40.4%; Score 953.5; DB 1; Best Local Similarity 42.6%; Pred. No. 2.6e-58; Matches 205; Conservative 89; Mismatches 156;
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A;Molecule type: DNA
A;Residues: 1-630 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04015.1; GSPDB:G
A;Experimental source: strain C-125
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the scrA gene encoding the sucrose-specific
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R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Invicio Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A; Reference number: A83650; MUID: 20263314
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C;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                           ΙΙ
                                                                        A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-480 < WMG.
A.Residues: 1-480 < WMG.
A.Cross-references: EMBL:X69800; NID:g407905; PIDN:CAA49461.1; PID:g407908
C.Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                                                                                                                                                                                                                                                                                                                                                                HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
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                                                                                                                                                                                                                                                                                                                                                                                    1 MAMVFPSLVNGYDVAATMAAG-EMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: BH0296
C;Superfamily: phosphotransferase system enzyme II sucrose-specific;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.7%; Score 701; DB 2; I
Best Local Similarity 51.4%; Pred. No. 4.7e-41;
Matches 146; Conservative 49; Mismatches 81;
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A)Gene: scrA
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
C;Keywords: phosphotransferase; sugar transport system
F;480-632/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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PSEGKLFSPVSGMVTALYPTHHALGITT----DRGAELLIHIGLDTVQLDGKFFTAHTIQ 577
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                                        GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSCHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI
                                                                                                                                                                 phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific NAlternate names: sucrose-specific enzyme II C; Species: Streptococcus sobrinus A; Variety: strain 6715 C; Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-M C; Accession: $68599 F; Chen, Y.Y.M.; Lee, L.N.; Lealanc, D.J. Infect. Immun. 61, 2602-2610, 1993 A; Title: Sequence analysis of scrA and scrB from Streptococcus sobril A; Reference number: $68598; MUID:93273516 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-632 <</ri>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                   (EC 2.7.1.69), sucrose-specific enzyme II
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PTS system, sucrose-specific IIBC component VCA0653 [imported] -
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%; Score 673; DB 2; Length 63: 36.4%; Pred. No. 5.5e-39; ive 76; Mismatches 197; Indels
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C;Genetics:
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Best Local Similarity 36.4%
Matches 168; Conservative
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                                             | : : | |::|| || : || EDDKKEPSASEEIKSPLKGEVVPLTEVQDHVFSSGAMGKGVAVRPKEGRLVAPINGTVTS 531
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                                                                                                                                                                                                                                                         AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                                                                                                                                              ::|:|:|| | : || | :::|| SLVYPTLV------VLTEGE-PLYTLFTGTIFESPVHITFLGIPVILMSYATSVIPIIL 234
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                                                                                                  SI----DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEA 297
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Matches 163; Conservative
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, A.; Galizci, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Sand, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seand, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference. number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: bglP
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
F;458-609/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-287, F', 289-433, G', 435,'S', 437-448,'HR', 451-548,'M',550-551,'S',553-60 A;Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB15963.1; PID:926364 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sucrose uptake protein - Vibrio alginolyticus
N;Alternate names: enzyme II:sucrose protein
C;Species: Vibrio alginolyticus
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 18-Jun-1999
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 18-Jun-1999
C;Accession: JQ0781
R;Blatch, G.L.; Scholle, R.R.; Woods, D.R.
Gene 95, 17-23, 1990
A;Title: Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose uptake-A;Reference number: JQ0781; MUID:91071601
A;Reference number: JQ0781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFPPIELELFNOGG-SFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGI
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Best Local
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Cyspecies
Cyspecie
C; Accession: F82432
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
R; Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
N; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Reference number: A82035; MUID:20406833
A; Residues: I-479 cHEI>
A; Residues: I-479 cHEI>
A; Residues: I-479 cHEI>
A; Residues: CB: AE004395; GB: AE003853; NID: 99658068; PIDN: AAF96554.1; GSPDB: GNOO1
C; Genetics:
A; Gene: VKA0653
A; Gene: VKA0653
A; Gene: VKA0653
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beta-glucoside permease - Bacillus subtilis
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Query Match
Best Local Similarity 33.8
Matches 154; Conservative
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:Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
A:Status: preliminary
A:Molecule type: DDA
A:Residues: 1.479 cBLA
A:Residues: 1.479 cBLA
A:Residues: 1.479 cBLA
A:Cross-references: GB:M76768; GB:M30194; NID:g155261; PIDN:AAA27555.1; PID:g155262
C;Genetics:
A:Genetics:
A:Gene: scrA
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T47097
R;Yoshida, K.; Sano, H.; Seki, S.; Oda, M.; Fujimura, M.; Fujita, Y.
Mcrobiology 141, 337-343, 1995
A;Title: Cloning and sequencing of a 29 kb region of the Bacillus subtilis genor
A;Reference number: 224350; MUID:95219088
A;Reference number: 224350; MUID:95219088
A;Ression: T47097
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-609
A;Cross references: EMBL:D31856; NID:9603765; PIDN:BAA06652.1; PID:g603778
A;Gene: N17C
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotran
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                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein N17C [imported] - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T47097
                                                                                                                                                                                                                                                                                                   KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                        VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                                                                                                                                          PVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQ 132
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                                                                                                                                                                                                                             MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH,60
                                                                                                                                                                                                                                                                                                                                                                                                                                              KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
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                                                                                                                                                           Length 479;
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                                                                                                                                                       Ouery Match 27.3%; Score 646; DB 2; Length 47 Best Local Similarity 46.5%; Pred. No. 2.9e-37; Matches 128; Conservative 54; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 645; DB 2; Length 60 ilarity 33.6%; Pred. No. 4.5e-37; Conservative 86; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 LGVVSIDAPDMVMFLVCA-VVTFFIAFGAAIAYGL 270
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Best Local Simi
Matches 154;
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera F;479-631/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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C; Species: Erwinia chrysanthemi
C; Date: 04 Sep-1998 #sequence_revision 04 Sep-1998 #text_change 16-Jul-1999
C; Accession: B42603
B; El Hassouni, M.; Henrissat, B.; Chippaux, M.; Barras, F.
J. Bacteriol. 174, 765-777, 1992
A; Title: Nucleotide sequences of the arb genes, which control beta-glucoside utilizat olase family including enzymes from eubacteria, archeabacteria, and humans.
A; Reference number: A42603; MUID:921211114
A; Accession: B42603
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beta-glucoside-specific phosphotransferase system-dependent permease - Erwinia chrysa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVS 241
TEPAMYGVNMRLKKPFAAALIGGAAGGAFYGMTGVASYIVGGNAGLPSIPVFIGPTFIYA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-631 <ELL.>
A; Cross-references: GB:M81772; NID:g148385; PIDN:AAA24814.1; PID:g148387
A; Note: sequence extracted from NCBI backbone (NCBIN:77535, NCBIP:77537)
                                                                                                                                                                                                                                                   465 HSPIKGEVKALSEVKDGVFSAGVMGKGFAIEPEEGEVVSPVRGSVTTIFKTKHAIGITS-
                                                                                                                                                                                                                                                                                                                                                                                   PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF
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                                                                                                                  311 QAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTK
                                                                                                                                                                                                                                                                                                                                            AEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPI
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Live 86; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 VVSNYKK--TGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
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Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Galizzi, J. Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardino A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, R.; Sekiguchi, J.; Sekowska, A.; Sea akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wight, A.; Tamamaco, H.; Yasumoto, K.; Yata, K.; Yoshida A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshkawa, H.; Danchin, A. Arcession: C69725
A; Status: nucleic acid sequence of the Gram-positive bacterium Bacillus subtill A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-139,'S',141-362,'L',364-464,'G',466-470 <SC2>
A,Cross-references: EMBL:254245; NID:g1000450; PIDN:CA91014.1; PID:g1000451
C;Comment: This enzyme functions as the specific trehalose transporter. It belongs
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C; Superfamily: phosphotransferase system sucrose-specific enzyme II, factor C; Superfamily: phosphotransferase; sugar transport system
C; Kywords: phosphotransferase; sugar transport system
C; Id-13-131/Domain: transmembrane #status predicted <TM1>
F; 160-181/Domain: transmembrane #status predicted <TM2>
F; 230-245/Domain: transmembrane #status predicted <TM4>
F; 230-245/Domain: transmembrane #status predicted <TM5>
F; 230-326/Domain: transmembrane #status predicted <TM5>
F; 305-325/Domain: transmembrane #status predicted <TM5>
F; 375-395/Domain: transmembrane #status predicted <TM7>
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Matches 116; Conserv
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R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. in press, 2001
A; Role complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Accession: D86807
A; Status: preeliminary
A; Molecule type: DNA
A; Residues: 1-636 <STO>
A; Reperimental source: strain IL1403
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:
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                                                                                                                                                                                                                                                                                                                                             hypothetical protein ptbA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphotransferase
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24.9%; Score 588.5; DB 2; Length
Best Local Similarity 33.5%; Pred. No. 3.8e-33;
Matches 148; Conservative 76; Mismatches 185; Indels
                                                                KAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL
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A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Reference number: A64720; MUID:97426617
A; Actatus: proliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-625 <BLAT>
A; Residues: 1-625 <BLAT>
A; Experimental source: GB:AE000449; GB:U00096; NID:92367269; PIDN:AAC76745.1; PID:917901
A; Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                      A Gene: bglF; bglS
C, Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
C, Keywords: phosphoprotein; phosphotransferase; transmembrane protein
E; 473-625/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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Best Local Similarity 30.8%
Matches 142; Conservative
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                                                                                                                                                                           C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C; Accession: H8326
C; Accession: H8326
N; Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masul, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Fritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A8356; MUID: 20263314
A; Accession: H8326
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-470 <STO>
A; Cross-references: GB: AP001514; GB: BA000004; NID: g10174613; PIDN: BAB05935.1; GSPDB: GNOC
C; Genetics:
A; Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
                                                                                                                                                              trehalose-specific enzyme II, BC component BH2216 [imported] - Bacillus halc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.1%; Score 569.5; DB 2; Best Local Similarity 42.9%; Pred. No. 5.4e-32; Matches 112; Conservative 55; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 VSIDAPDMVMFLVCAVVTFFI 260
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Status: preliminary
Molecule type: DNA
Molecule type: Molecule type:

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Gaps

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US-09-604-231-2
2363
1 MAMVFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP 468
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           322656 seqs, 67552660 residues
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                           Searched:
                                                                                              Run on:
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322656

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/paa/USO6\_NEW\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/paa/USO8\_NEW\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/paa/USO8\_NEW\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/USO9\_NEW\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/paa/USO9\_NEW\_COMB.pep:\*

7: /cgn2\_6/ptodata/1/paa/USO9\_NEW\_COMB.pep:\*

8: /cgn2\_6/ptodata/1/paa/USO9\_NEW\_COMB.pep:\*

8: /cgn2\_6/ptodata/1/paa/USO0\_NEW\_COMB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	PCT-US02-03987-13467	US-09-815-242-13467	US-10-072-851-13467	US-09-897-516-6783	PCT-US02-03987-5658	US-09-815-242-5658	US-10-072-851-5658	PCT-US02-03987-12270	US-09-815-242-12270	US-10-072-851-12270	PCT-US02-03987-10809	US-09-815-242-10809	US-10-072-851-10809	US-09-897-516-6540	PCT-US02-03987-12272	US-09-815-242-12272	US-10-072-851-12272	PCT-US02-03987-13794	US-09-815-242-13794	US-10-072-851-13794	PCT-US02-03987-5822	US-09-815-242-5822	US-10-072-851-5822	PCT-US02-03987-12942	US-09-815-242-12942
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Length	627	627	627	473	619	619	619	681	681	681	484	484	484	473	484	484	484	455	455	455	687	687	687	719	719
Query Match	27.9	27.9	27.9				14.6		•	14.6	14.3	14.3	14.3	14.1	13.7	13.7	13.7	12.9	12.9	12.9	12.7	12.7	12.7	12.7	12.7
Score	099	099	099	396	345.5	345.5	345.5	345.5	345.5	345.5	338.5	338.5	338.5	334	323	323	323	305.5	305.5	305.5	300	300	300	300	300
Result No.	7	7	е	4	'n	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE 298

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SEQ ID NO 13467
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                        AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPYGGLLFGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/242,578
PRIOR PAPLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-16
SOFTWARE: FASTERQ for Windows Version 4.0
SEQ ID NO: 14407
                                                                                                    AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 660; DB 6; I 34.3%; Pred. No. 8.1e-41; Live 92; Mismatches 187;
                                                                                                                                                                                                                  ; Sequence 13467, Application US/09815242; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13467
                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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Best Local Simi
Matches 159;
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APPLICANT:
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
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                                                                                               AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
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-APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV 357
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                          239 VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE
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Best Local Similarity 34.3%; Pred. No. 8.1e-41;
Matches 159; Conservative 92; Mismatches 187;
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus pneumoniae US-10-072-851-13467
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
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Ohlsen, Kari L.
Zyskind, Judith W.
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Roemer, Terry
Jiang, Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LTFIAIGPAMRWVGDVLAHGLQ----GLYDFGGPVGGLLFGLVYSPIVITGLHQSF---- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSEKLKGLAGASGVSA----VLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 KPENKKVVAGLMGSAALTSFLTGITEPLEFSFLFVAPLLFFI---HAVLDGLSFLTLYLL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 DKQSQAVTASATELPYAVLEAMGGKANIKHLDACITRLRVEVNDKSKVDVPGLKDLGASG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFL----ITPVLTLLTGF 82
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: ProKaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.4e-17
                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 345.5; 24.2%; Pred. No. 1.4
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5658
LENGTH: 679
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                                                                                                                                                                                                                                            ; ORGANISM: Staphylococcus aureus
PCT-US02-03987-5658
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Yamamoto, Robert T.
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Zyskind, Judith W
Wall, Daniel
Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 132; Conservative
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
CIRE REFERENCE: ELITRA.026
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hosing, Osceph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spridonov, Sergel.
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
SEQ ID NO 6783
SEQ ID NO 6783
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                                                                                                           AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                    418 AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
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; ORGANISM: Xenorhabdus sp.
US-09-897-516-6783
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US-09-897-516-6783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 WFEFGSWKNAAGEIIHGDQRIFIEQIREGAHLTAGKFMQGEFPVMMFGLPAAALAIYHSA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 679;
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   192;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.6%; Score 345.5; DB 6
Best Local Similarity 24.2%; Pred. No. 1.4e-17;
Matches 132; Conservative 68; Mismatches 192
                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
         PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/265,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus aureus
US-09-815-242-5658
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648 PIIVT 652
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APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 KSEKLKGLAGASGVSA----VLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 227
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                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
FRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 5558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRGANISM: Staphylococcus aureus
US-10-072-851-5658
                                                                                                         Zyskind, Judith W. Wall, Daniel
Trawick, John D. Yamamoto, Robert T.
Foulkes, J. Gordon
Zamudio, Carlos
Haselbeck, Robert
Ohlsen, Kari L.
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Matches 132; Conservative
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Jiang, Bo
Boone, Charles
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IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVR 368
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                                                                                                         Genes
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Pred. No. 1.4e-17
                                                                                                         Essential
                                                                                                                                                         FILE KREFERNIA. UITA. UITA.
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-12-27
PRIOR FILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRALESEQ for Windows Version 4.0
SOFTWARE: 601
                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus aureus US-09-815-242-12270
  Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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                                                                                                                                              FILE REFERENCE: ELITRA.011A
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Best Local Similarity
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                                                                            APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FAPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 681;
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                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12270
LENGTH: 681
                                     Sequence 12270, Application PC/TUS0203987 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus PCT-US02-03987-12270
OLT 8
-US02-03987-12270
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PIIVT 654
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Gaps

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APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA 0.28 VPC
CURRENT APPLICATION NUMBER: PCT/USO2/03987
CURRENT APPLICATION NUMBER: PCT/USO2/03987
CURRENT FILING DATE: 2002-02-02
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
369 TKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTT 428
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Mismatches 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 338.5; DB 1 Pred. No. 2.9e-17;
                                                                                                                                                                                                                                                                                   Sequence 10809, Application PC/TUS0203987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10809, Application US/09815242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Enterococcus faecalis PCT-US02-03987-10809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick.
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.011A
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PCT-US02-03987-10809
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Best Local 9
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US,10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                          Sequence 12270, Application US/10072851
GENERAL INFORMATION:
                                                                                                                                                                                              APPLICANT: Carr, Grant J.
APPLICANT: V.H. Howard
APPLICANT: Eoulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: House APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Chlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-12270
                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
Jiang, Bo
Boone, Charles
                429 PIVVS 433
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10-072-851-12270
                                                         650 PIIVT 654
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APPLICANT:
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APPLICANT: Goldman, Barry S.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorrhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)8
CURRENT FILING NATE: 2000-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                    259 EKQLHKIVPESIDIIVTPTISLLVIGLATIFLIMP----VAGAISNGLVGIINVVLEKGG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 PVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG-SFIFATASMANIAQGAACLAVFFL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 RLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
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                                                                                                                                                                                                                                                                                                                                                                                                   2 AMVF---PSLVNGYDVAATMAAG---EMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATI 55
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                                                                                                                                                                                                                                                                                           14.3%; Score 338.5; DB 7; Length 33.2%; Pred. No. 2.9e-17; Live 54; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL 270
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10809
LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6540, Application US/09897516; GENERAL INFORMATION:
                                                                                                                                                                                     ; ORGANISM: Enterococcus faecalis
US-10-072-851-10809
                                                                                                                                                                                                                                                                                                                      Best Local Similarity 33.2%
Matches 94; Conservative
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SEQ ID NO 6540
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Best Local Similarity
Matches 77; Conserv
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APPLICANT: Boone, Charles
APPLICANT: Bose, Charles
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITHA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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33.2%; Pred. No. 2.9e-17;
Live 54; Mismatches 114;
                      CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-110-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-10-21
PRIOR PILING DATE: 2001-10-31
PRIOR PILING DATE: 2001-10-31
     CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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GENERAL INFORMATION:
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TT: Ohlsen, Kari L.
TT: Zyskind, Judith W.
TT: Wall, Daniel
TTawick, John D.
NT: Yamamoto, Robert T.
NT: Roemer, Terry
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
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Best Local Similarity 33.2%,
Matches 94; Conservative
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Sequence 12272, Application PC/TUS0203987

SEQUENCE 12272, Application PC/TUS0203987

GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of TITLE OF INVENTION: Proliferation
FILE REFRENCE: ELITRA 10280PC
CURRENT APPLICATION NUMBER: PCT/US02/03987

CURRENT FILING DATE: 2002-02-02

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 15811

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12272

LENGTH: 484
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122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                  GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
                                                                                      69 FLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVIT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 SIDAPDMVMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDATAAPVPAGTTKA 295
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; ORGANISM: Staphylococcus aureus
PCT-USO2-03987-12272
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Best Local Similarity 32.29
Matches 96; Conservative
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PCT-US02-03987-12272
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418 NI 419
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Search completed: March 21, 2002, 16:27:36 Job time: 337 sec

Sequence 2, Appli Patent No. 5254799 Patent No. 5254799

Sequence 6, Appl Sequence 10, App

Appli

Sequence 4 Sequence 4 Sequence 1 Sequence 2

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Sequence 7, Appli
Sequence 13, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
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APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
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US-09-231-818-21
US-08-836-325-16
US-08-678-039A-40
US-08-960-048-10
US-09-120-513-2
US-09-450-105-2
5254799-6
                                                                                                                                                                                                                                                                                            US-08-446-486-7
US-08-446-486-6
US-08-446-486-6
US-08-157-363A-10
US-08-463-308-6
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PCT-US93-11405-10
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5523211-1
US-08-810-720-13
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2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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ZIP: 32606
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/07828788A Patent No. 5273746
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TELECOMMUNICATION: INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
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IMMEDIATE SOURCE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SA
STREET: 2421 N.W. 41st
        528
1969
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ORIGINAL SOURCE
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US-07-828-788A-12
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        STATE:
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488.023 Million cell updates/sec
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Sequence 1, Appli
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Sequence 2, Appli
Sequence 12, Appli
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Patent No. 5164180
Patent No. 5188960
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                                                                                                                                                                                                                                                                                                                                                   1 MAMVFPSLVNGYDVAATMAA......IEAGANLLNVAKKEAVPATP 468
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                                                                                                                                                                                        March 21, 2002, 16:20:49; Search time 21.58 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-911-364-1
US-08-464-700-2
US-08-836-325-2
US-08-836-325-10
US-08-836-325-10
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US-08-801-344-9
US-09-498-599-9
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-08-510-646B-22
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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COMPUTER:
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TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
                                                                    13;
                                                                                                                                                                                                ---AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
                                                                                                                                                                                                                                                 337 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 396
                                                                                                                                                                                                                                                                                   494 DILRITSPGOISTL---RVTITAPLSQRYRVRIRY--ASTINLOFHTSIDGRPINGGNFS 548
                                                                                                                                                                                                                                                                                                                       397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                549 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 593
                                                                    Gaps
                                  Length 1176;
                                                                    Indels
                                                                                                      249 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-
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SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,034
                              ; Score 113.5; DB 1;
; Pred. No. 0.019;
43; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/210,110
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SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
CLASSIFICATION: 435
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APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08356034
Patent No. 5691308
GENERAL INFORMATION:
APPLICANT: PAYRE, Jewel M.
                                4.8%;
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                                                                    Conservative
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MEDIUM TYPE: Floppy
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                                                 Similarity
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594 YIERIEFVPA 603
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COUNTRY:
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US-08-356-034-2
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Sequence 2, Application US/08933891
Patent No. 6096708
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                             LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: 811A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8%; Score 113.5; DB 1;
22.4%; Pred. No. 0.019;
11ve 43; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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STREET: 2421 N.W. 41st Street, Suite A-1
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        STRAIN: AIZAWAI.
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 22.48;
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(904)372-5800
                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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FILING DATE:
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594 YIERIEFVPA 603
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                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
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295 AEA-----EAP-----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 LFVLDGTEFSFASLTADLPSTIY -- RQRGTVDSLDVIPPQDNSVPARAGFSHRLSHVTML 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1176;
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4.8%; Score 113.5; DB 5; Length
Best Local Similarity 22.4%; Pred. No. 0.019;
Matches 56; Conservative 43; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARX: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
                                                                       COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: APACHIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
FILING DATE: 19921231
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904,375-8100
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-040-751-1
Sequence 1, Application US/08040751
; Patent No. 5407825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES
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                STREET: 2421 ...
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594 YIERIEFVPA 603
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                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US92-11337-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 AEA-----EAP----AEFSN---DSTIIQAPLIGEAIALSSVSDAMFASGKLGS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVAIVPIKGQLVSPVSGKIVVAFPSGHAFAVRIKAEDGSNVDILMHIGFDTVNLNGTHFN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
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4.8%; Score 113.5; DB 3; Length 1176;
Best Local Similarity 22.4%; Pred. No. 0.019;
Matches 56; Conservative 43; Mismatches 96; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF SEQUENCES: 16
CORRESPONDENCE: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
                                                                                                                                                                                                                                                                                                                                              MA43.C1.D1
                                             US/08/210,110
                                                                                                   PELLING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
PELLING DATE: 14-DEC-89
PRIOR APPLICATION NUMBER: 07/311,955
PRIOR APPLICATION NUMBER: 07/311,955
PILING DATE: 27-UON-89
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOMOR: (904)372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
APPLICATION NUMBER: US/08/356,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: BACILLUS THURINGIENSIS
                                                                                     JMBER: 07/865,168
09-APR-92
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                          APPLICATION NUMBER:
                                                                                   APPLICATION NUMBER:
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594 YIERIEFVPA 603
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ORIGINAL SOURCE:
                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US92-11337-12
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108 AGVKPGKVPGVGLPGV-----YPGGVLP------GARFPGVG------ 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 TTGKLP-YGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPGVGGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GVPGVPGAI-PGIGGI-----AGVGTPAAAAAAAA--AKAAKYGAAAGLVPGGP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL----
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                                                                                                                     APPLICANT: RCTHSTEIN, Aser
APPLICANT: REELY, Fred W.
APPLICANT: RCHELY, Fred W.
APPLICANT: RCHELY, Fred W.
APPLICANT: ROTHSTEIN Steven J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
NUMBER OF SEQUENCES: 8
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 731;
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 108.5; DB 2;
; Pred. No. 0.03;
47; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bent, Stephen A. REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 041082/0104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,552
FILING DATE: 07-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                           ; Sequence 1, Application US/08911364
; Patent No. 5969106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.6%
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-911-364-1
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                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                          US-08-911-364-1
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                 APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
TITLE OF INVENTION: Lepidopteran-active Toxins
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4:8%; Score 113.5; DB 1; Length 1179; 22.4%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                           ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA39.C1.D3
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFEXX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS THURINGIENSIS AIZAWAI
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: PS811 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES
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597 YIERIEFVPA 606
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GENERAL INFORMATION:
                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                         STATE: FI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CLONE: 1
US-08-040-751-1
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Matches 5
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Peripheral Nervous System Specific Sodium Channels, DNA Encoding Therefor, Crystallization, X-ray Diffraction, Computer Molecular Modeling, Rational Drug Design, Drug Screening, and Methods of Making and Usin Thereof
                                                                       ---GARFPGVG----- 140
                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                          364 GVGVGGIPTYGVGAGGFPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 -----VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASG-KLGSGV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 KAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDT------VNL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 GVAPGVG--VAPGIG-----PGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 NG------LCEFD 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 PGLGVGGGVPGLGVGGGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGA 595
                                                                                                                  76 TLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL-VYSPIVITGLHQSF 134
                                                                                                                                                                                                          135 PPIELELFNOGGSFIFATASMANIAOG------AACLAVFFLAKSEKLKGLAGA 182
                          16 ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVL 75
                                                                                                                                               198 TTCKLP-YGYGPGGVAGAAGKAGYPTCTGVGPQAAAAAAAAAKFGAGAAGVLPGVGGA
                                                                                                                                                                                                                                                                                                                                                257 -GVPGVPGAI-PGIGGI-----AGVGTPAAAAAAAA--AKAAKYGAAAGLVPGGP
                                                                                                                                                                                                                                                                                                                                                                                             .....GVVSIDAPDMVMFL
                                                                                                                                                                                                                                                                                                     183 SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SIDPDATAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 IDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KESSLER, GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 ---VCAVVTFFIAFGAAIAYGLYLVRRNG-------
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FILING DATE: 2-MAY-1997
                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral N
TITLE OF INVENTION: Sodium Chann
TITLE OF INVENTION: X-ray Diffra
TITLE OF INVENTION: Drug Design,
TITLE OF INVENTION: Thereof
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Patent No. 6110672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-08-836-325-2
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                                                                                                                                                                                          362 GVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAA 421
                                                                -----VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASG-KLGSGV 338
                                                                                                             422 KAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGV 481
                                                                                                                                                           339 AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDT-----VNL 390
                                                                                                                                                                                                                                                        -----THFNPLKKQGDEVKAGEL-----LCEFD 415
                                                                                                                                                                                                                                                                                              534 PGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSSQHLPSTPSSPRVPGA 593
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                                                                                                                                                                                                                                                                                                                                                                             416 IDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/464,700
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.6%; Score 108.5; DB 4;
Best Local Similarity 20.6%; Pred. No. 0.03;
Matches 122; Conservative 47; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6232458
GENERAL INPRMATION:
APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL6520
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL9661
FILING DATE: 28-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DET_AU93/00655
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08464700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GHC
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TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-464-700-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19477
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-464-700-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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STATE:
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GOLDSTEIN & FOX P.L.L.C
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PatentIn Release #1.0, Version #1.30
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                                                                                   N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0917.0240002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 4.6%; Score 108;
Similarity 20.7%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILLING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
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                                                              3: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,203
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: not relevant not relevant
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      Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/33
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1989 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ludwig, Steven R
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    TITLE OF INVENTION: The NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                               USA
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                                                                ADDRESSEE:
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                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-836-325-12
                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                     STREET:
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Best Local Si
Matches 91;
                                                                                                        CITY:
STATE:
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APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 IFDLVINQA-FDITIMVLICLNMVTMMVEK-----EQQTEYMDYVLHWINMVFIILFTG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECVLKLIS------LRH-----YYF--TVG---WNILYFVVVILSIVGMFLAEMIEK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 FLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPYGGLLFGLYYSPIVITGLHQSFPPIELEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | : : : | : | : | 647 Y-----FVSPTLFRVIRLARIGRILRL-----IKGAKGIRTLLFALMMSLPALFNIGL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 RLRWPFFI----GIGTAA------IGGALIALFNIKAVALGAAGFLGVVS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              860 IAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGE-GGEMDSLRSQMEERFMSANPS 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 FNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%; Score 108; DB 3 20.7%; Pred. No. 0.055;
                                                                                                                                                                                                                          0917.0240002
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LUMWIG, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
                                                                                                                                                                                               REFERENCE/DOCKEY NUMBER: 36,203
REFERENCE/DOCKEY NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 GTHFNP----LKKQGDEVKA 407
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                                                                                                                                                                                                                                                                                                                                             1011 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-836-325-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                               LENGTH:
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20; 1602 Y-----FVSPTLFRVIRLARIGRILRL----IKGAKGIRTLLFALMMSLPALFNIGL 1649 1561 ECVLKLIS------LRH----YYF--TVG---WNILYFVVVILSIVGMFLAEMIEK 1601 1650 LLFLVMFIYALFGMSNFAYVKKEAGINDMFNFETFGNSMICLFQITTSA-GWDGLLAPIL 1708 VATEESTEPLSEDDFEMFYEVWEKFDPDAT-----QFIEFCKLSD--FAAALDPPLL 1814 --- DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS 278 FLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL 141 FNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNL 201 202 RLRWPFFI----GIGTAA------IGGALIALFNIKAVALGAAGFLGVVS 241 IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGV 338 339 AIVPTKGQLVS----PVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL---MHIGFDTVNLN 391 28 LFGLDVAQAGYQGTVLPVLVVSWILLATIEKFLHKRLKGTADFL-----ITPVLTLLLTG Indels 114; Length 1989;

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1707 NSAPPDCDPKKVHPGSSVEGDCGNPSVGIFYFVSYIIISFLVVVNMYIA----VILENFS 1762
                                                                          1597 IEK----YFVSPTLFRVIRLARIGRILRL-----IKGAKGIRTLLFALMMSLPALFNIGL 1647
                                                                                                                                                                                                                                                                                                                                    ---LRH-----YYF--TVGWNIFDFVVVILSIVGMFLA-----EM 1596
                                                                                                                                                                                                                                                                                                       279 IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGV 338
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                                                                                                                              202 RLRWPFFI----GIGTAA------IGGALIALFNIKAVALGAAGFLGVVS
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TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
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Best Local Similarity 22.45
Matches 56; Conservative
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597 YIDRIEFVPA 606
  1559 ECVLKLIS--
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5164180-6
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5188960-2
; Patent No. 5188960
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5164180-6
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                                                                                                                                                                                                                                                                                                                                             Peripheral Nervous System Specific Sodium Channels, DNA Encoding Therefor, Crystallization, X-ray Diffraction, Computer Molecular Modeling, Rational Drug Design, Drug Screening, and Methods of Making and Using Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
82 FLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 LFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFL-----ITPVLTLLLTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.5%; Score 107; DB 3; L. Best Local Similarity 20.7%; Pred. No. 0.2; Matches 91; Conservative 66; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New York Ave., N. W., Suite 600 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0917.0240002
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APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
                                                                                                                                                                                                            Sequence 10, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gall
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                     : | | ||:: :|| |
1874 KVSYEPITTTLKRKQEEVSA 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                          392 GTHFNP----LKKQGDEVKA 407
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                                                                                                                                                                                                                                                                                                                    APPLICANT: BOLDON, LAURENTION: PeriTILE OF INVENTION: SodiTITLE OF INVENTION: X-TETLE OF INVENTION: Drug TITLE OF INVENTION: The NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3934
COMPUTER READABLE FORM:
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US-08-836-325-10
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E: DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: RNCROBIAL ITITLE OF INVENTION: FROM SUGAR NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                     4.5%;
                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1864 amino acids
                                                                                                                                                                                                                                               Conservative
                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
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                                                                                   amino acid
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Best Local Similarity
Matches 94; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                                                                           US-08-804-227C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AEA-----EAP----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 DILRRTSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINOGNFS 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                          380 LFVLDGTEFSFASLTADLPSTIY -- RORGTVDSLDVIPPODNSVPARAGFSHRLSHVTML 437
                                                                                                                                                                                                                                                                                                                            Length 1179;
                  ; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE ; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                    249 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                       4.5%; Score 106.5; I
22.4%; Pred. No. 0.1;
iive 42; Mismatches
                                                      | LEPIDOPTERAN ACTIVE TOXINS | LEPIDOPTERAN ACTIVE TOXINS | LEPIDOPTERAN ACTIVE TOXINS | LEPIDOPTERAN APPLICATION DATA: | APPLICATION NUMBER: US/07/451,261 | FILING DATE: 14-DEC-1989 | PRIOR APPLICATION DATA: | APPLICATION NUMBER: 371,955 | FILING DATE: 27-JUN-1989
APPLICANT: PAYNE, JEWEL; SICK, AUGUST J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                          LENGTH: 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-804-227C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                         Query Match
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62 RL-------KGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQG 105
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                                                                                                                                                                                                                                                            346 ALLATYGTART---AERPLWLGSLKSNIGHTQAAAGVAGVIKMVLAMR------HG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 LYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AVFFLAKŠEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI---A 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 RAQAARLYDALTGTGTGTGTGQGAGQG-------AGPGTAEVAGALAHART 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 LFNIKAVALGA-----AGFLGVVSIDAPDMVMFLVCAVV----TFFIAFG-----AAIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 YGLYLVRRN------GSIDPD-----ATAAPVPAGTTKAEAEAPAEFSN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 QTALFRLAEHHGLRAEALCGHSVGEIAAAH---AAGVLTLPDAARLVA-ARGRLMQALPA 696
                                                                                           Gaps
                                                                                                                                                                     7 SLVNGYDVAATMAAGEMPMW----SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                              393 RLPRTLHVDRPTTRVDWEKGGVRLLTEPV-------PWPGEAGEPRRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFRHRAVVLGGNRAELLAGLRELAEEEHPGPRVVTGTAPATERRTAFLFSGQGSQRAGSG
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    Length 1864;
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; Score 106.5; DB 2;
; Pred. No. 0.2;
45; Mismatches 159;
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8000 Excelsior Drive, Suite 401
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 TIFGPDTGNVGWILLAMVIGGAIGIRLAKKVEMTEMPELVAILHSFVGLAAVLVGFNSYL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 HHD-AGMAPILVNIHLTEVFLG----IFIG-AVTFTGSVVAF-------GKLCG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LVYS-PIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 KISSKPLMLPNRHK-------MINIAALVVSFLLLIVFVRTDSVGLQ- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 LAGASGVSAVLGITEPA-IFGVNLRLRWPFFIGIGTAAIGGA----LIALFN-IKAVALG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AAGFMLSNDLLIVTGALVGSSGAILSYIMCKAMN--RSFISVIAGGF-----GTDGSS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 TAAPVPAGT-TKAEAEAPAE-FSNDSTIIQAPLTGEAIA----LSSVSDAMFASG---K 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKA---------EDGSNVDI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : | : | 342 FG------IHPVAGRL-----PGHMNVLLAEAKVPYDIVLEMDEINDDFADTDT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 151; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QGTVLPVLV-----VSWILATIEKFL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 462;
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pyridine nucleotide transhydrogenase, subunit ORGANISM: B
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5%; Score 105.5; DB 3;
21.1%; Pred. No. 0.029;
ive 66; Mismatches 123;
                 ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2106
TELEPAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 SLFGLDVAQAGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21.19
Matches 91; Conservative
                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
CLASSIFICATION: 435
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60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----OGTVLPVLV-----VSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 105.5; DB 4; Length 462;
; Pred. No. 0.029;
66; Mismatches 123; Indels 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pyridine nucleotide transhydrogenase, subunit ORGANISM: B US-09-498-599-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKA------
                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REPERNCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 SLFGLDVAQAGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANGE TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
COUNTRY: U.S.A. ZIP: 53717-1914
                                                                                                                                                                                                                                                   CLASSIFICATION:
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Search completed: March 21, 2002, 16:23:16 Job time: 147 sec

us-09-604-231-2.rai

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                                                                                                                                                                                                March 21, 2002, 16:19:04 ; Search time 42.58 Seconds
   (without alignments)
814.145 Million cell updates/sec
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2363
1 MAWYFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP 468
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(SIDSB/gcgdata/geneseq/geneseqp/Ant)81. DAT:

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(SIDSB/gcgdata/geneseq/geneseqp/Ant)83. DAT:

(SIDSB/gcgdata/geneseq/geneseqp/Ant)84. DAT:

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(SIDSB/gcgdata/geneseq/geneseqp/Ant)88. DAT:

(SIDSB/gcgdata/geneseq/geneseqp/Ant)89. DAT:
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ñ	Description	C. qlutamicum phosp	C glutamicum prote	Brevibacterium lac	C.qlutamicum phosp	C glutamicum prote	C.glutamicum phosp	Escherichia coli p	C.qlutamicum phosp	B. burgdorferi ant	Amino acid sequenc	B. burgdorferi ant
SUMMARIES		07	50	80	80	07	21	82	23	12	20	13
SUMM		AB66707	AG92650	AB69080	AB66708	6932	B667	AAG98282	AB66723	AY20012	AY53620	AY20013
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Query Match
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                                      phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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                                                                                                                                                                                                                                                                                                                                                                               synthesis; vitamin; saccharide;
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                                                                                                                                    Length 468;
                                  present invention relates to Corynebacteium glutamicum
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                                                                                                                                                     Indels
                                                                                                                                   100.0%; Score 2363; DB 22; 100.0%; Pred. No. 7.7e-228;
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                                                                                                                                                    0; Mismatches
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                Claim 4; Page 101-102; 144pp; English,
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transformation
                                                                                                                                            Similarity
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Matches 46
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The present invention provides a number of nucleotide and protein asquences from the Corpreform bacterium Corynebacterium glutamicum. These sequences from the Corpreform bacterium, one of a gene derived from a mutant of coryneform bacterium, measuring expression amount and amalyshing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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100.0%; Pred. No. 1.3e-227
                                                                                                                                    Σ
                                                                                                                               S, Hayashi
Ozaki A;
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Ikeda M,
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                                                                                     KYOW ) KYOWA HAKKO KOGYO KK
                  2000JP-0159162.
2000JP-0280988.
99JP-0377484
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Senoh A,
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nes 468; Conserv
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                  07-APR-2000;
03-AUG-2000;
16-DEC-1999;
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Tateishi |
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362 AA;
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sucrose PTS (phosphoenoflyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and have improved amino-acid and nucleic acid productivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
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                                                                                                                                                        phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system.
                                                                                                         Brevibacterium lactofermentum sucrose PTS enzyme II protein SEQ ID
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Pred. No. 1.6e-224;
4; Mismatches 3;
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                 ¥Ÿ.
              AAB69080 standard; Protein; 661
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Matches 461; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Sugimoto M,
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N-PSDB; AAF32543.
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sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
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                                                                                                   360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate:
AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
                                                                                                                                                                                                       SCHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to Corynebacteium glutamicum
                                                                                                                                                                                                                                                                                                                                                       661
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                                                                                                                                                                                                                                                                                                                                421 AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sugar phosphotransferase system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.1%; Score 1821; DB 22; 100.0%; Pred. No. 9.6e-174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.glutamicum phosphoenolpyruvate protein #2.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 104-106; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB66708 standard; protein; 362
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99US-0150310.
99DE-1042095.
99DE-1042097.
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Matches 362; Conservative
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Gaps

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Length 683;

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from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                        87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                                                                                                                                                                                                                      27 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI 86
                                                                                                                                                                                                                                                                         146 GSFIFRATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 ELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
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dplitfdadfirskdlplitpvvvsnaakfgeiegipadqanssttvikvngk
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                                                                                                                                                                                   Score 468.5; DB 22; Length
Pred. No. 6.3e-38;
); Mismatches 206; Indels
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                                                                                                                                                                                     19.8%;
29.8%;
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99US-0150310.
99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 FGAAIAYGLYLVRRNGSID-
                                                                                                 European Patent Office
                                                                                                                                                                                                      Similarity
                                                                                                                                    683 AA;
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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Matches 141;
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                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                  286
                                                                                                                   AGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
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                                 VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                                   KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
 ydfggpvggllfglvyspivitglhqsfppielelfnqggsfifatasmaniaqgaacla
                                                  Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 29; SEQ ID NO: 6961; 246pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG93207 standard; Protein; 683 AA.
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2000JP-0280988.
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Senoh A,
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N-PSDB; AAH68426.
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07-APR-2000;
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tp 362
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Tateishi N
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                                                                  Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation
                                                                                                                                                        The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                           87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
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                                                                                                                                                                                                                                                                                                                                                            SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI 86
                                                                                                                                                                                                                                                                                                                                                                                                                           456 mflvlald---yrsneerdearakvaadkqaeedlkaeanatpaapvaaagagagagag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 PAGTTKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLV
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                                                                                                                                                                                                                                                                                                            DB 22; Length 683;
                        Haberhauer
                                                                                                                                                                                                                                                                                                          19.8%; Score 468.5; DB 22; 29.8%; Pred. No. 6.3e-38; Ive 79; Mismatches 206;
                        Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli protein sequence SEQ ID NO:330.
                         ij
                       Schroeder
                                                                                                                                   Claim 32; Page 136; 144pp; English.
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Best Local Similarity 29.89
Matches 141; Conservative
                         B,
                         Kroeger
                                              WPI; 2001-080989/09
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(BADI ) BASF AG
                       Pompejus M,
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The present invention describes a purified or isolated nucleic acid sequence (1) consisting essentially of one of the 93 nucleotide sequences given in AARB1202 to AARB1294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(1) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (1) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacterial. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of schementary to a complementary to a complementary to be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganism species in contact the particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular species of microorganism can be used as probes of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes of microorganisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 glvggaaynrwsdiklpdflsffggkrfvpiatgffclvlaaifgyvwppvghaihagge 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 --GSFIFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis;
bacterial gro⊮th inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IAIGPAMRWVGDVLAHGLQGLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 F --- GGPVGGLLFGLVYSPIVITGLHQSFPPI---------ELELFNQG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVL-----TLLLTGFLTF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-457376/49
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH81338
                                                                                                                                                                                                                                                                 WO200148209-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001
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Tue Mar 26 10:32:38 2002

Length 135;

Query Match

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sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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345 viffaiyfvvfslvirmfnlktpgredkedeivteeansnteegltglatnyiaavggtd 404
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                                                                     324
                                                                                                                                                                                                                            SDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIG 384
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                                                                                                                                                                                                                FDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate:
                                                                                                                        265 AIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSV
                                                                                                                                                                          ----GFLGVVSIDAPDMVMFLVCAVVTFFIAFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoenolpyruvate; sugar phosphotransferase system; PTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                            C.glutamicum phosphoenolpyruvate protein #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; Page 142-143; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                             AAB66723 standard; protein; 135 AA
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99US-0150310.
99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum
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03-SEP-1999;
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221
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                                                          326 DAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGF 385
                                                                                                                 386 DIVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYG 445
                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Borrelia burgdorferi nucleic acids – used to develo products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                           Antigenic protein; vaccine; Lyme disease; infection; detection.
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9.9%; Score 234; DB 22;
llarity 37.5%; Pred. No. 1.7e-15;
Conservative 25; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lathigra
                                                                                                                                                                                                                                                                                                                                                                B. burgdorferi antigenic protein, f346.aa.
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                                                                                                                                                                                                                                                                          AAY20012 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi GH, Erwin AL, Hanson MS,
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                          446 LGEIEAGANLLNVAKK 461
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                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi.
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              Local Similarity
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20-JUN-1997;
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22-JUL-1997
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291 GTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSP 350
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                                                                                                                                                                                                                                                                                                                                                                                               176 salresnekttlkqvfkvlgqndqllwlafaywfyglgintlnalqlyyfsyilgdargy 235
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3 fiitnlitairigevlldplignaidrtesrwgkfkpwvvgggiisslallalftdfggi 62

    used to develop

                                                                 ----PVGGL-LFGLVYSPIVI -----TGLHQSFPPIELE-----LFNQGGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 VTFF---IAF-----GAAIAYG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY20013 standard; Protein; 135
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97US-0050359.
97US-0053344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 ALIALFNIKAVALGAAGF----
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22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant Lactobacillus bulgaricus strain lacking beta-galactosidase activity useful for making fermented milk products, especially yoghurt
319 IALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVD 378
                                                                                                                           379 ILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKT 438
                                                                                                                                                                       | :| | :|:|||| | | :::| || ||:::| |:::| ||:|::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:
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22.2%; Pred. No. 2.1e-14;
Live 74; Mismatches 154; Indels 211; Gaps
                                     Amino acid sequence of a permease encoded by the lactose operon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactose operon; permease; beta-galactosidase; mutant; yoghurt; beta-galactosidase activity; lactose fermentation; fermented milk product; Streptococcus thermophilus.
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Matches 125; Conservative
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                                                                                                                                                                                                                                                             439 GPVNTYGLGEIE 450
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117 ssie-ysfgrle 127
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N-PSDB; AAZ36227.
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related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

413 AA;

Sequence

SSXS

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                                                                 This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in mannans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                            353 GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 412
                                                                                                                                                                                                                                                                                            products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
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                                                                                                                                                                                                                       Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphoenolpyruvate; sugar phosphotransferase system; PTS.
                                                                                                                                                                                                                  7.0%; Score 166.5; DB 20; Length
84.7%; Pred. No. 9.7e-09;
Ive 21; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                 413 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIE 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphoenolpyruvate protein #6.
                                                                                                                                                                                                                               34.7%; Prea. ....
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                                        Page 161; 275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAB66722 standard; protein; 413
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99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                                                   34; Conservative
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                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yping or identify; or transformation
                                                                                                                                                                               135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.glutamicum
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03-SEP-1999;
                                        Claim 12;
                                                                                                                                                                               Sequence
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The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or

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Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome.
                                                                                                87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                              that,
                                                                                                                                                 146 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL 201
                                                                                                                                                             Gaps
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                                                 SLFGLDVAQAGYOGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a Staphylococcus aureus protein, based on homology with a human or Staphylococcus aureus protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - to isolate antimicrobial compounds, and in vaccines against S.
                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 1..126
/note= "residues designated X are not defined
the specification"
   Length
                          Indels
                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of Staphylococcus aureus protein.
 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DJC,
JM;
                          93;
7.0%; Score 166.5; DB 2
28.9%; Pred. No. 5.1e-08;
ive 35; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles I
Ward JN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Pages 432-433; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson JE, K
Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                    AAW28051 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US02318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0011888
                                                                                                                                                                                                                                                                                                                                     (first entry)
            Best_Local Similarity 28.99
Matches 54; Conservative
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Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-424969/39.
N-PSDB; AAT84002.
                                                                                                                                                                                                202 RLRWPFF 208
                                                                                                                                                                                                                        398 rfkktyf 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus infection
                                                                                                                                                                                                                                                                                                                                    27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1996;
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Pratt JM,
 Query Match
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believed to be a nerve growth factor or ptsG protein. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in EScherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81501 to AAV81679 represent specifically claimed protein sequences lated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent cifically claimed nucleotide sequences isolated from S. pneumoniae. sequences have antibacterial and antiinflammatory properties.
                                                                                                                                                                                                                                                                                                                                        334 LGSGVAI-VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                  58 kgfkyfvngndhveaggtxlqfdqgyiqqxgynadxivvis-----nsadlgkvelt 109
                                                                                                                                                                                                                                                                                                                                                                                                            393 THFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAG 452
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                            44; Indels 13;
                                                                                                                                                                                                                                                                     DB 18; Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae type 4 protein sequence #56.
                                                                                                                                                                                                                                                                 6.8%; Score 161.5; DB 1
32.8%; Pred. No. 2.8e-08;
ive 25; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY81556 standard; Protein; 449 AA
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.8'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumococcal disease.
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                                                                                                                                                                                                                126 AA;
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specifically (
The sequences
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                                                                                                                                                                                                                  Sequence
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The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful for the diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianaemic, gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 PAIFGV----ALRERWPFFIG-IGTAAIGGALIALFNIKAV-----ALGAAGFLGVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 mmktvts1keg----aviadg----wam-gnvvarfgttgiftaiimaivtv11yrmcvk 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 LFNQGGSFIFA--TASMANIAQGAA-----CLAVFFLAKSEKLKGLAGASGVSAVLGITE 193
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                        1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQG-----TVLPVLVV---- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | | | ::| || |: || || || 294 --aagghfavagefsnmfviaggsgatlglclylafaskseglkaigrasvvpalfnine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 hnwvikmpeavpegvsrg-----ftalvpgfvvafvvifingllvamgtdifkvia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ipfgfvsnltnswiglmilylltgllwivgihganivfafv-splalanmaen-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            49 -SWILATIEKFLHKRLKGTADFLITPVLTLLTGFLT------FIAIGPAM----
                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                      Length 449;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF555 polypeptide sequence SEQ ID NO:1110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID 280
                                                                                                                                                                                                                                                                                                                 Mismatches 117;
                                                                                                                                                                                                                                                                      Score 156; DB 21;
Pred. No. 6.5e-07;
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                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                          6.6%;
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                              449 AA;
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                                                                                                                                                                                                                                                                                                               85;
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Query Match
Best Local Similarity 32.7%; Pred. No. 1.2e-07;
Bast Local Similarity 32.7%; Pred. No. 1.2e-07;
Matches 32; Conservative 19; Mismatches 43; Indels 4; Gaps
Qy 300 PAEFSNDETIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 359
Db 14 psslkpsslkivaplggilvpldqvpdpvfaqkmvgdgisldpisnellapvagtvtqlh 73

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Search completed: March 21, 2002, 16:22:45 Job time: 221 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                              - protein search, using sw model
                                              protein
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1 MAMVFPSLVNGYDVAATMAA......IEAGANLLNVAKKEAVPATP 468 US-09-604-231-2 2363 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

hits satisfying chosen parameters: of Total number

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SUMMARIES	y Franth DR ID Description	1 PTSA_PEDPE P4347	664 1 PTSA_STRMU	480 1 PTSB_STAXY	474 1 PTSB_PASMU Q9cjz2	609 1 PTBA_BACSU P40739	479 1 PTSB_VIBAL	631 1 PTBA_ERWCH P26207	470 1 PTTB_BACSU	625 1 PTBA_ECOLI	456 1 PTSB_SALTY P08470	456 1 PTSB_KLEPN . P27219	674 1 PTGA_CORGL Q45298	459 1 SACX_BACSU P15400	460 1 PTSB_BACSU	473 1 PTTB_ECOLI P36672	699 1 PTGA_BACSU	651 1 PTAA_KLEPN P45604	6 648 1 PTAA_ECOLI P09323	324 1 PTGA_BACST P42015	631 1 YBFS_BACSU P39816	4 485 1 PTDA_ECOLI	8 189 1 PTGA_BORBU	8 168 1 YPQE_BACSU P50829	8 634 1 LACY_STRTR	6 474 1 YFEV_ECOLI P77272	6 154 1 PTGA_MYCCA P4561	168 1 PTGA_ECOLI P08837	482 1 PTSB_VIBCH	3 168 1 PTGA_SALTY P02908	165 1	9 627 1 LACY_LACDE P22733	
																							189	168								•	
dР	Query Match I	44.8			28.7		27.3																ω.	ω,					10.3	_			
	Score	1058.5	953.5	701	678	657	646	640	570	567.5	492	489	462.5	406	390	367	321.5	317.5	298.2	294.5	287.5	270.5	256	255	254.5	250.5	249.5	24	244.5	244	238.5	233	
	Result No.	7	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	ç

P43466 pediococcus P47315 mycoplasma	048624 leuconostoc P32154 escherichia P54745 escherichia	P54715 bacillus su P32672 escherichia	P23355 xanthomonas P57635 buchnera ap	P75039 mycoplasma P24400 lactobacill
RAFP_PEDPE PTGA_MYCGE	LACY_LEULA PTVB_ECOLI HRSA_ECOLI	PTIB_BACSU PTWC_ECOLI PTER_PUCCA	PTFB_XANCP PTMA_BUCAI	PTFA_MYCPN PTLB_LACCA
641 908	639 483 658	359 359 578	5,6 580 632	694 577
4.0	7.0 6.7 6.4	5.8	4.4.	5.2
221	165.5 159 151.5	144.5	126.5	122 120.5
35	36 37 38	3.0 4.0 1.0 1.0	4 4 4	44 45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PPEL.0;
Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G.;
Submitted (XXX-1994) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRNVATE-DEPENDENT
-:- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRNVATE-DEPENDENT
-:- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRNVATE-DEPENDENT
-- SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-- TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SKIDAR SITE
-- AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
-- PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
-- PHOSPHORYLATION SITE (THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-SYSTEM, SUCROSE-SPECIFIC IIABC COMPONENT (EIIABC-SCR) (SUCROSE-PERMENSE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                       Pediococcus pentosaceus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
-:- SUBCELLULAR LOCATION: INTEGRAL BRABRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EILA DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILC DOMAIN.
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InterPro; IRRO11917; PTS_EIIA.
InterPro; IRRO11996; PTS_EIIA.
InterPro; IRRO11996; PTS_EIIA.
InterPro; IRRO1352; PTS_EIIA.
InterPro; IRRO3356; PTS_EIIA.
InterPro; IRRO3376; PTS_EIIA.
InterPro; IRRO377; PTS_EIIA.
InterPro; PTS_EIIA.
InterPro
                                                                         651 AA
                                                                         PRT;
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                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1255;
                                                                     PTSA_PEDPE
P43470;
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RESULT 1
PTSA_PEDPE
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us-09-604-231-2.rsp

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                                                                                                                              KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                121 VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                                                              540
                                                                                                     Gaps
                                                                                                                    MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 13, Last annotation update)
PTS 5VSTEM, SUCROSE-SPECIFIC INABC COMPONENT (EIIABC-SCR) (SUCROSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                 AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoenolpyruvate-dependent sucrose phosphotransferase system.";
                                                                                                                                                                                                                        KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                          LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE
                                                                                                                                                                                                                                                                     VAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI
                                                                                                                                                                                                                                                                                                                                       Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; "Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans
                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                  649
                                                                                                                                                                                                                                                                                                                                                                 467
                                 HOSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
C87BA09D550A7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAKKEAVPAT
                                                                                                     Mismatches 151; Indels
                                                                                   1;
                                                                                    Score 1058.5; DB Pred. No. 1.2e-62;
      EIIB DOMAIN.
EIIC DOMAIN.
EIIA DOMAIN.
PHOSPHORYLATION (
PHOSPHORYLATION (
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                            44.8%; Sc.
46.7%; Pred
78; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 171:263-271(1989).
Transmembrane
                                                          68454 MW;
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                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                       651
25
324
562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus mutans
                                                         651 AA;
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Phosphorylation;
                       510
25
324
562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-GS-5;
                                                                                                     221;
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                                       MOD_RES
MOD_RES
SEQUENCE
        DOMAIN
DOMAIN
DOMAIN
MOD_RES
                                                                                  Query Match
                                                                                           Local
                                                                                           Best Loc
Matches
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6
                 374 YFLIKDKKMKGLSSSSGVSALLGITEPALFGVNLKYRFPFFCALIGSASAAAIAGLLQVV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 MIMVAPGAANIIGLAANAPISKAATIGAYTGFWNIFGLHVTQASYTYQVIPVLVAVWLLS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 TIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 GGLLFGLVYSPIVITGLHQSFPPIELEL --- FNQG---GSFIFATASMANIAQGAACLAV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAMVFPSLVNGYDVAATMAAGEMP-----MWSLFGLDVAQAGYQGTVLPVLVVSWILA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GMGVFGALYSPVVMTGLHQSFPAIETQLISAFQNGTGHGDFIFVTASMANVAQGAATFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSPHORYLATION (BY SIMILARITY).
OSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
809E63E32281A9A1 CRC64;
                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIB DOMAIN.
EIIC DOMAIN.
EIIA DOMAIN.
PHOSPHORYLATION (:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pram; Pr00358; PTS_EIIA_I; 1.
Pram; Pr00367; PTS_EIIB; 1.
Pram; Pr02378; PTS_EIIE; 1.
Pr0Dom; PD001476; PTS_EIIB; 1.
Pr0Dom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA, 1.
PROSITE; PS01035; PTS_EIIA_1; 1.
MEDLINE=93329360; PubMed=8336109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
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HSSP; P08837; 2F36.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001352; PTS_EIIE.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Transmembrane
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Best Local Similarity
Matches 205; Conserv
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331
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MOD_RES
SEQUENCE
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for commercial
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                                                   340
                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-BERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
              547
                                                                                                                          603
                                                                                                                                                  OGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY-GLGEIEAGANLLNVA 459
                                                                                                                                                                            663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR - PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                 VPAGTTKAEAEAPAEFSNDST-----IIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                                                                341 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
                                                                                                               604 ADQKIKKGDVLGTFDSDKIAEAGLDNTTMFIVTNTADYASVETLASSGTVAVGDSLLEVK
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                          480 AA
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIB; 1.
Probom; PD001476; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB.75: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-DSM 20267 / C2A;
MEDLINE-94049686; Pubmed-8232209;
                                                                                                                                                                                                                                                                                                                  (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X69800; CAA49461.1;
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1288;
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                                                                                                                                                                                                                                                                                                                01-0CT-1996
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P51184;
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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Fro. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

FURTION: THIS IS A COMPONENT OF THE PHOSPHOENCEPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT POPHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLOGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUCROSE-
BC COMPONENT)
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                     1 MAMVFPSLVNGYDVAATMAAG-EMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                     KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                                                                                                                  8;
                                EIIB DOMAIN.
ELIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
AB4E1D9785D84E47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                              DB 1; Length 480;
                                                                                                                                                                                                81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, 16C 2.7.1.69) (EII-SCR).
SCRA OR PTSB OR PM1846.
 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: PROTÉIN N-PHOSPHOHISTIDINE + PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN
Sugar transport; Tra
ne; Phosphorylation.
                                                                                                                                                            ; Score 701; DB 1;
; Pred. No. 3e-39;
49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                     Inner membrane;
                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE SUGAR (BY SIMILARITY)
                                                                                                                                                            Query Match 29.7%;
Best Local Similarity 51.4%;
Matches 146; Conservative 4
Phosphotransferase system;
                                                                                                         51326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                   480
26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella multocida
                                                                                                       480 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                   26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PM70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTSB_PASMU
                                                                                                         SEQUENCE
                                  DOMAIN
DOMAIN
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9CJZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
PTSB_PASMU
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                                                                                                                                                                                                                                                                                                                                                              KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                       VYSPIVITGLHQSFPPIELELFNQ----GGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                      177 KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF 236
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                                                                                                                                                                                                                                                                                                                          1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                       Interrio, ipp03352; ..._
Interro; IPR003352; ..._
Pfam; PF0367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB _ CYS; FALSE_NEG.
Phosphotransferase system; Transferase; Sugar transport; Plasmid; Transmembrane; Inner membrane; Phosphorylation; Complete proteome. DOMAIN 109 474 BIIC DOMAIN.

DOMAIN 109 474 BIIC DOMAIN.

178 POTENTIAL.

- TRANSMEM 109 129 POTENTIAL.
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P40739; Q45661;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-BGL)
(BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
D26FA1A059603C01 CRC64;
                                                                                                                                                                                                                                                                                   28.7%; Score 678; DB 1; Length 474; 49.5%; Pred. No. 9.7e-38; Indels ive 51; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 269
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                                            EMBL; AE006222; AAK03930.1; -. InterPro; IPR001996; PTS_EIIB. InterPro; IPR003352; PTS_EIIC.
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es 135; Conserv
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-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM, THE IICD DOMAINS CONTAINT THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IID DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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those
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MEDLINE=95189730; PubMed=7883710;
le Coq D.G., Lindner C., Krueger S., Steinmetz M., Stuelke J.;
"New beta-glucoside (bgl) genes in Bacillus subtilis: the bglp product has both transport and regulatory functions similar to of BglF, its Escherichia coli homolog.";
J. Bacteriol. 177:1527-1535(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96204517; PubMed-8628237;
Beloin C., Hirschbein L., le Hegarat F.;
"Suppression of the Bg1+ phenotype of a delta hns strain of
Escherichia coli by a Bacillus subtilis antiterminator binding
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-i- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-i- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-i- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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Transmembrane; Complete proteome.
41 EIIB DOMAIN.
609 EIIA DOMAIN.
25 PHOSPHRYLATION (BY S
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InterPro: IPR001127; PTE_EIIA.
InterPro: IPR001137; PTE_EIIA.
InterPro: IPR001352; PTE_EIIC.
Pfam; PF00376; PTE_EIIA.1; 1.
Pfam; PF00376; PTE_EIIA; 1.
ProDom; PD001476; PTE_EIIE; 1.
ProDom; PD001476; PTE_EIIE; 1.
PROSITE; PS000371; PTE_EIIB; 1.
PROSITE; PS01035; PTE_EIIA; PTE_EIIA;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168 / BGSC1A1;
MEDLINE-95219088; PubMed-7704263;
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EMBL; D31856; BAA06552.1; --
EMBL; D29985; BAA06256.1; --
EMBL; X85408; CAA59697.1; --
EMBL; Z99124; CAB15963.1; --
PIR; S47174; --
HSSP; P20166; 1AX3.
Subtilist; BG10934; bg1P.
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DOMAIN 1
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Mol. Gen. Genet.
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                                                                                                                                  repressor-encoding gene (scrR).";
Gene 101:45-50(11991).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
THE SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose
                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
PROTEIN HISTIDINE + SIGAR PHOSPHATE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMYFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
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                                                                                                   Blatch G.L., Woods D.R.; "Nucleotide sequence and analysis of the Vibrio alginolyticus
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PHOSPHORYLATION (BY SIMILARITY).
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FBF906B5170E3EB7 CRC64;
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46.5%; Pred. No. 1.3e-35;
Live 54; Mismatches 87; Indels
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Pfam: PF02378; PTS_EIIC; 1.
ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
PROSPOCTANSFORMS System; Sugar transport; Tra
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SEQUENCE OF 1-12 FROM N.A.
MEDLINE=91285433; PubMed=2060795;
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InterPro; IPR003352; PTS_EIIC.
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EMBL, M35009; AAA27557.2; -.
PIR, JQ0781; JQ0781.
HSSP, P05053; 11BA.
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Matches 128; Conservative
                   uptake-encoding region."
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BC COMPONENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFPPIELELFNQGG-SFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGA-AGFLGVVSIDAPDMVMF
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                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                         Length 609;
                                                                                                                                                                                                                                                                                                                                        84; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II,
                                                                                                                                                                                                                                                      5F630C671D21FBED CRC64;
                                                                                                                                  A -> S (IN REF. 3).
L -> F (IN REF. 2).
E -> G (IN REF. 2).
A -> S (IN REF. 2).
DG -> HR (IN REF. 2).
I -> M (IN REF. 2).
G -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                       27.8%; Score 657; DB 1; 33.4%; Pred. No. 3.1e-36;
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MEDLINE=91071601; Pubmed=2174811;
Blatch G.L., Scholle R.R., Woods D.R.
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                                                                                                                                                                                                                                                       64550
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Best Local Similarity 33.4%
Matches 153; Conservative
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609 AA;
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P22825;
01-AUG-1991 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Hassouni M., Henrissat B., Chippeux M., Barras F.;

"Nucleotide sequences of the arb genes, which control beta-glucoside utilization in Erwinia chrysanthemi: comparison with the Escherichia coli bgl operon and evidence for a new beta-glycohdrolase family including enzymes from eubacteria, archeabacteria, and humans.";

J. Bacteriol. 174:765-777(1992).

-I. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANEERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPERBASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS IN PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS PHOSPHORYLATION SITE (THE DONOR IN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ÁCTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                                                                           01-MAY-1992 (Rel. 22, Created)
10-MAY-1992 (Rel. 22, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, BETA-GLUGOSIDES-SPECIFIC ITABC COMPONENT (EITABC-BGL)
(BETA-GLUCOSIDES-PERMEASE ITABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON ARBG (BY SIMILARITY).
                                                                                                                                                                                                                                                                                        Erwinia chrysanthemi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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SIMILARITY)
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Pfam: PF00367; PTS_EIIA_1; 1.
Pfam: PF00367; PTS_EIIA_1; 1.
Probom: PD00243; PTS_EIIB; 1.
Probom: PD002243; PTS_EIIB; 1.
PROSITE: PS00371; PTS_EIIA_1; 1.
PROSITE: PS01035; PTS_EIIA_1; 1.
PROSITE: PS01035; PTS_EIIA_1; 1.
PROSITE: PS01035; PTS_EIIA_1; 1.
PROSIDE: PS01035; PTS_EIIA_1; 1.
PROSIDE: PS01035; PTS_EIIA_1; 1.
PROSIDE: PS01035; PTS_EIIA_1; 1.
PROSIDE: PS01035; PTS_EIIA_1; 1.
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MEDLINE-92121114; PubMed-1732212;
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InterPro; IPR00127; PTS_EIIA.
InterPro; IPR01996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
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                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                    Pectobacterium.
                                                                                    PTBA_ERWCH P26207;
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PTBA_ERWCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 VIPPTGVDSSVWAAVIGTLLAFRFAALTSWSFGVPKD---ETQPAAADSPA--VLAETQA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LVHPSMIAAFN---AMQAPDHSTLHFLGIPITFINYSSSVIPILFASWVSCKLEKPLNRW 240
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STRAIN=168 / MARBUGG,
MEDLINE=9704649; Pubmed=8917076;
Schoeck F., Dahl M.K.;
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                              3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PITE_BACSU
PATTH:
P3774, 034771;
01-FEB-1995 (Rel. 31, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE PTS SYSTEM, TREHALOSE-PECIFIC IIBC COMPONENT (EIIBC-TRE)
COMPONENT) (EC 2.7.1.69) (EII-TRE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVS
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                                                                                                                                                                                                                                                                                                                                        Length 631;
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                                                                                                                                                                                                                                                                                                                                                                                  86; Mismatches 200;
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                                                                                                                                                                                                                                                                                                                                     27.1%; Score 640; DB 1; 33.8%; Pred. No. 4.2e-35;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein."; Gene 194:191-199(1997).
                                                                                                                                                                                                                                           Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40 6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
Microbiology 142:3057-3065(1996).
                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR - PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EILC DOMAIN.
genes encoding a putative specific enzyme IITre and a potential regulator of the trehalose operon."; Gene 175:59-63(1996).
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                                                                                                                               STRAIN=AC327;
MEDLINE-97417488; PubMed-9272861;
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                                              STRAIN=AC327;
MEDLINE=97124190; PubMed=8969503;
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EMBL; D83967; BAA23409.1; -.
EMBL; D86417; BAA22289.1; -.
EMBL; X80203; CAA56494.1; -.
EMBL; Z99108; CAB12609.1; -.
HSSP; P05053; 11BA.
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257 TPEGIQLLVVAPITLLLTGFASFIIIGPITFAIGNVLTSGLISVFGSFAALGGLLYGGFY 316
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"Nucleotide sequence of bglC, the gene specifying enzymeIlbgl of the PEP: sugar phosphotransferase system in Escherichia coli Kl2, and overexpression of the gene product.";
J. Gen. Microbiol. 133:563-573(1987).
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schnetz K., Toloczyki C., Rak B.;
Bett-glucoside (bgl) operon of Escherichia coli K-12: nucleotide
sequence, genetic organization, and possible evolutionary
relationship to regulatory components of two Bacillus subtilis
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1-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (FIIABC-BGL)
PETA-GLUCOSIDES-FERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
BGLF OR BGLC OR B3722.
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                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                         Score 570; DB 1; Length 470; Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                                    99; Indels
                                                                                                                                    -> S (IN REF. 1).

-> L (IN REF. 1 AND 4).

-> G (IN REF. 1 AND 4).

7A741850A2697D53 CRC64;
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[3]
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                                                                                                       SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARROHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SIGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                               Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                 R EMBL; AL0325; AAA02073.1; -.

R PIR; A25977; C25977.

R PIR; A47616; A47616.

R HSSP; P20106; LAX3.

R GCGene; EG10115; bglF.

R InterPro; IPR001926; PTS_EIIA.

R InterPro; IPR001935; PTS_EIIA.

R InterPro; IPR00335; PTS_EIIB.

R Pfam; PF00378; PTS_EIIB; 1.

R Pfam; PF00378; PTS_EIIB; 1.

R Pfam; PF00378; PTS_EIIB; 1.

R PTODOM; PD001476; PTS_EIIA; 1.

R PROSITE; PS001371; PTS_EIIA; 1.

R PROSITE; PS001371; PTS_EIIA; 1.

R PROSITE; PS001371; PTS_EIIA; 1.

R PROSITE; PS01037; PTS_EIIA; 1.
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
MEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli
                                                                                                                                                                                   FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON BGLG.
CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL BEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                    genome: organizational symmetry around the origin of replication.";
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Ebner R., Lengeler J.W.; "DNA sequence of the gene scrA encoding the sucrose transport protein "DNA sequence of the gene scrA encoding the sucrose transport protein EnzymeII(Scr) of the phosphotransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Bgl) proteins."; MOI. Microbiol. 2:9-17(1988).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 YSPIVITGLHQSFPPIELELFN-QGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA
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                                                                                                                        17;
Length 625;
                                                                                                                               Indels
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REAGFDLTTPVLISNSDDFTDVLPHGTAQISAGEPLLSIIR 625
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      DB 1;
                                                                                                                  91; Mismatches 211;
Score 567.5; DB 1
Pred. No. 2.5e-30;
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MEDLINE-91100329; PubMed-1846143;
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MEDLINE-88216186; PubMed=3285123;
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      24.0%;
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                                                                                                                               Conservative
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      Query Match
Best Local Simi
Matches 142;
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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                                                                                              J. Bacteriol. 173:449-456(1991).

-! FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE ILCD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN THE SUGAR BINDING SITE PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO THE SUGAR. BIBG-SCR BELONGS TO THE EIIBC DOMAIN TYPE AND LACKS A COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EII-SCR-MEDIATED PHOSPHORYLATION OF SUCROSE REQUIRES THE ACTIVITY OF ENZYME IIABCHORYLATION OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

-!-CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR — PROTEIN HISTIDINE + SUGAR — PRO
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                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE. SIMILARITY: CONTAINS A PTS EIIB DOMAIN. SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport; Plasmid;
Hardesty C., Ferran C., Direnzo J.M.;
"Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of scrY, the structural gene for a phosphoenolpyruvate-dependent sucrose phosphotransferase system
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PHOSPHORYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

98A6F1620AE50885 CRC64;
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Transmembrane; Inner membrane; Phosphorylation.
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InterPro: IPR003352; PTS_EIIC.
Pfam: PF00376; PTS_EIIE; 1.
ProDom: PD001476; PTS_EIIB; 1.
PR0SITE: PS01035; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X67750; CAA47973.1; -. EMBL; Y00541; CAA68605.1; ALT_SEQ. EMBL; M38416; AAA98418.1; -. PIR; S01036; WQEBST. HSSP; P05053; 1IBA.
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Best Local Similarity 38.5
Matches 104; Conservative
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309
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STRAIN=1033-5P14/ KAY2026;

X MEDLINE=91312133; PubMed=1649946;
A Schmid K., Ebner K., Jahreis K., Lengeler J.W., Titgemeyer F.;
A Schmid K., Ebner K., Jahreis K., Lengeler J.W., Titgemeyer F.;
The state of the portion, Scry, is involved in sucrose uptake in enteric bacteria."; 1-914-950(1991).

I MOLIND MICROBIOLIS 1941-950(1991).

I MOLIND MICROBIOLIS 19540-950(1991).

C -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSFERATION SITE OF THE SIGAR BINDING SITE AND THE TRANSFERE IT TO THE SUGAR. BILLO-SCR BELONGS TO THE EIIB DOMAIN TYPE AND LACKS A COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EII-SCR-MEDIATED COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EII-SCR-MEDIATED PHOSPHORYLATION OF SUCROSE REQUIRES THE ACTIVITY OF ENZYME IIA-
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                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-SCR).
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Klebsiella.
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  456 AA
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InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X57401; CAA40658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00367; PTS_EIIB;
Pfam; PF02378; PTS_EIIC;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1164
220
220
320
330
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340
448
448
300
300
                                                                                                                                                                                                                                                        Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; $15195; $15195.
HSSP; P05053; 1IBA.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1144
1181
1181
1209
2247
2380
3360
3360
3388
428
428
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=573;
PTSB_KLEPN
P27219;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262
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                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactofermentum phosphotransferase system.";
Submitted (NOV-1993) to the EMBL/Genbank/DDBJ databases.
-! FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                      236
                                                                                                                                              60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                             120 LVYSPIVITGLHQSFPPIELELFNQ---GGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                          358 KAITLPSAFSAMLGITEAAIFGINLRFVKPFIAALVGGAAGGAWVVSMHVYMTAVGLTAI 417
                                                                  Gaps
                                                                                           3 MVFPSLVNGYDVAA---TMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, GLUCOSE-SPETIFIC ILABC COMPONENT (EIIABC-GLC) (GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
                                                                                                                                                                                                                 177 KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and nucleotide sequence of enzyme II of Brevibacterium
                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUGAR
                                                                51; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                        Length
 4AFDF5405CAEFC66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum (Brevibacterium flavum).
                                      Score 489; DB 1;
Pred. No. 2.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                     674 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPONENT) (EC 2.7.1.69) (EII-GLC/EIII-GLC)
                                                                                                                                                                                                                                                                                                        LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                                                                                                                                  PGMAIVQASSLLNYIIGMAIAFAVAFALSL 447
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
48022 MW;
                                      20.7%;
38.5%;
                                                                104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
 AA;
                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 13869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1718;
 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pBSBG2
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (
01-NOV-1997 (
20-AUG-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                   PTGA_CORGL
Q45298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoon K.-H.
 SEQUENCE
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHE
                                                     Best Local
                                                                                                                                                                      338
                                                                                                                                                                                                                                                                                                                                                                                        PTGA_CORGL
                                                                Matches
                                                                                                                   186
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87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 EAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 TVFGLPMVLNDYSGOVFPPLIAAIGLYWVEKALKKIIPEAVOMVFVPFFSLLIMIPATAF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 YDFIQGPMGAWNFACFGLVTGVFLIALKEKNRAMRQVSLGGMLAGLLGGISEPSLYGVLL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PDATAAPV------PAGTTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTSMLLVLFFDYRSDAERDEAKAQMAAAEQTNNTPAAPAAPVAPAAGAAAAGGAAGAT-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 VATKPRLAAGQLVEITSPLEGHAVPLSEVPDPIFAAGKLGPGIAIEPTGNTVVAPADATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY). SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67A75AAF76E42FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 462.5; DB 1;
Pred. No. 2.2e-23;
9; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 IDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                628 PEFIRSKNLPLITPVVVSNANKFGEIVGIEAAQADATTTVIKV
                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                               InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR00395; PTS_EIIC.
Pfam; PF00358; PTS_EIIA.
Pfam; PF00378; PTS_EIIA; 1.
Pfam; PF02378; PTS_EIIC; 1.
ProDom; PD001476; PTS_EIIA; 1.
PRODITE; PS00371; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA, 1.
PROSITE; PS00371; PTS_EIIA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGAAIAYGLYLVRRNGSID------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.6%;
EMBL; L18875; AAA22992.1;
HSSP; P08837; 2F3G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442
493
28
594
674 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 139; Conserv
                                                                                                                                                                                                                                                                                      542
1126
1126
1162
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260
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44
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or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *A gene encoding a tyrosine tRNA synthetase is located near sacS in Bacillus subtilis.";

DNA Seq. 1:251-261(1991)

-I- FUNCTION: COULD ACT AS BOTH A KINASE AND A PHOSPHATASE ON SACY

(BY SIMILARITY TO BGLF) AND THUS INACTIVATES SACY WHICH IS A TRANSCRIFTIONAL ANTITERMINATOR THAT REGULATES LEVANSUCRASE AND LEVANASE SYNTHESIS.

AND LEVANASE SYNTHESIS.

-I- SIMILARITY: CONTAINS A PTS EIIE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of the sacS locus of Bacillus subtilis reveals the presence of two regulatory genes."; Gene 90:153-155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochlnsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
Rapoport G., Danchin A.;
Raposit I. Santana B. Sant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIIB DOMAIN.
EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaser P., Kunst F., Debarbouille M., Vertes A., Danchin A., Dedonder R.;
                                                                                                                                                                                                                                                                                                                                                                                                 Zukowski M.M., Miller L., Cogswell P., Chen K., Aymerich S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          !ranscription regulation; Transferase; Phosphorylation;
                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
02-AUG-2001 (Rel. 40, Last annotation update)
NEGATIVE REGULATORY PROTEIN OF SACY.
459 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95020537; PubMed-7934828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92216127; PubMed-1806041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001476; PTS_EIIB; 1. PROSITE; PS01035; PTS_EIIB_CYS; 1
                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE-90337338; PubMed-2116367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M29333; AAA75335.1; -.
EMBL; X52480; CAA36719.1; -.
EMBL; X73124; CAA51570.1; -.
EMBL; Z99123; CAB15867.1; -.
PIR; JU0293; JU0293.
PIR; S16421; S16421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001996; PTS_EIIB. InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 348-459 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02378; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subtilist; BG10560; sacX
                                                                                                                                                                       SACX OR SACS OR IPA-14R.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P05053; 11BA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinmetz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168;
SACX_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
MOD_RES
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PERSINE STAIN 168;

MEDLINE-95020537; PubMed=7934828;

MEDLINE-95020537; PubMed=7934828;

MEDLINE-95020537; PubMed=7934828;

MEDLINE-95020537; PubMed=7934828;

MILIO M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,

Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,

Rapoport G., Danchin A.;

Rapoport G., Danchin A.;

"Bacillus subtilis genome project: cloning and sequencing of the 97

kb region from 325 degrees to 333 degrees.";

MOI. Microbiol. 10:371-384(1993).

-! FUNCTION: THES IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT

-! FUNCTION: THES IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
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TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 09, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PPTS SYSTEM, SUCROSE-SECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (BC 2.7.1.69) (EII-SCR).
SACP OR IPA-49D.
                                                                                                                                                                                                                                                                                                                                                       206 IWGLHIPMMGYQGSMIPILLSVFVMSKIEKLLKSIVPKSLDVVIIPFITVMVTGCLALIV 265
                                                                                                                                                                                                                                                                            266 MNPAASIIGQIMTQSIVYIXDHAGIAAGALFGGIXSTIVLSGLHHSFYAIEATLLANPHV 325
                                                                                                                                                                                                                                                                                                                                                                                                              205 WPFFIGIGTA---AIGGALIALFNIKAVALGAAGFLGVVSIDAP------DMVMFLVC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                     386 RPF---IGAAIGGAIGGAYVVAVQVVANSYGLTG-IPMISIVLPFGAANFVHYMIGFLIA 441
                                                                                                                                      Gaps
                                                                                                                                                                            28 LFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIA 87
                                                                                                                                                                                                                                                                                                                                   GGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLR
                                                                                                                                                                                                                                                        IGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF---NQ
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Fouet A., Arnaud M., Klier A., Rapoport G.;
"Bacillus subtilis sucrose-specific enzyme II of the phosphotranse system: expression in Escherichia coli and homology to enzymes II from enteric bacteria."
Proc. Natl. Acad. Sci. U.S.A. 84:8773-8777(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON SACT
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
A5C4E996ECDA3D40 CRC64;
                                                                                               17.2%; Score 406; DB 1; Length 459; 37.9%; Pred. No. 7.7e-20;
                                                                                                                                      88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA
                                                                                                                                      47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus group; Bacillus
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                                      49024 MW;
                                                                                                                                      Conservative
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  136 1
433 4
459 AA;
                                                                                                               Best Local Similarity
Matches 96; Conserv
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
SIMILARITY: 57% IDENTITY WITH THE NEGATIVE REGULATORY PROTEIN OF SACY.
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PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.5%; Score 390; DB 1; Length 460; 44.6%; Pred. No. 8.7e-19; tive 34; Mismatches 69; Indels
 CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR
                                                                                                                                                                                                                                                                                                                                                                                 Phosphotransferase system; Sugar transport; Transferase; Transmembrane; Phosphorylation; Complete proteome.

DOMAIN

460

EIIC DOMAIN.

460
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6A303DC042BFE379 CRC64;
            PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DMVMFL----VCAVVTFFIAF 262
                                                                                                                                                                                                                                              PIR; A39938; A39938.
PIR; S39704; S3704.
HSSP; P06053; JIBA.
Sublitist; B610595; SacP.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001395; PTS_EIIC.
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Matches 91; Conserv
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473 AA.

PRT;

STANDARD;

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RESULT 15

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                                                                     PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-TRE).
            01-JUN-1994 (Rel. 29, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE-
                                                                                                                                                                                                                                        Klein W., Horlacher R., Boos W.;
"Molecular analysis of treB encoding the Escherichia coli enzyme II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR001352; PTS_EIIC.
Pfam; PF00378; PTS_EIIB; 1.
ProDom; PF003178; PTS_EIIB; 1.
ProDom; PS0101476; PTS_EIIB; 1.
ProSyrE; PS010135; PTS_EIIB; 1.
Phosphotransferase system; Sugar transport; Transferase;
Transmembrane; Inner membrane; Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                           MEDLINE-95334362; Pubmed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                     specific for trehalose.";
J. Bacteriol. 177:4043-4052(1995).
                                                                                                                                                                                                                         MEDLINE-95332210; PubMed=7608078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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EMBL; AE000495; AAC77197.1; -.
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                    Escherichia coli.
                                                                                                                                                               NCBI_TaxID=562;
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                  PHOSHORYLATION (BY SIMILARITY).
POTENTIAL.
GL -> PF (IN REF. 1).
GL -> PF (IN REF. 1).
GGTPILGIVUG -> AQRRSLVSCLA (IN REF. 2).
MISSING (IN REF. 1).
                                                                                                                                                            A -> 0 (IN REF. 1).
PGILSIQPSYWQVEALAMATAIIIPIVLTSFIYQRKYRLGT
LDIV -> NRLSDSTELLAGVCAGNGYRHHPDCTHLVYLS
AEIPPGHAGHCLIFFGAQLKSHSQE (IN REF. 1).
7437F8822B624944 CRC64;
                                                                                                                                                                                                                                                                                       60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLA----HGLQGLYDFGGPVGG 115
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                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 15.5%; Score 367; DB 1; Length 473;
Best Local Similarity 30.1%; Pred. No. 2.9e-17;
Matches 80; Conservative 63; Mismatches 109; Indels 14; Gaps
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 EIIB DOMAIN.
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045622 bacillus sp
199470 bacillus sp
199470 bacillus st
095323 staphylococ
095322 staphylococ
09512 vibrio chol
099243 staphylococ
099243 staphylococ
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099273 staphylococ
090374 staphylococ
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"Characterization of the divergent sacBK and sacAR operons, involved in sucrose utilization by Lactococcus lactis.";
J. Bacteriol. 181:1924-1926(1999).
EMBL: 297015; CAB096900.1; -.
HSSP; P45618; 2GPR.
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42.9%; Pred. No. 9.4e-47;
Live 89; Mismatches 145; Indels 36;
29£499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) EACYME II SUCROSE PROTEIN (EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 AA
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR00358; PTS_EIIC.
Pfam; PP00358; PTS_EIIA.; 1.
Pfam; PP00378; PTS_EIIB; 1.
Propom; PD002243; PTS_EIIR; 1.
PROSITE; PS00371; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                       09KBR9
046072
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MEDLINE=99173919; Pubmed=10074089;
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Best Local Similarity 42.99
Matches 203; Conservative
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Lactococcus lactis.
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NCBI_TaxID=1358;
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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                                                                              AEAEAPAEFSNDSTIIQ-----APLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ 346
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                                                               121 VYSPIVITGLHQSFPPIELELFNQ-----GGSFIFATASMANIAQGAACLAVFFLAKSE 174
                                                                                                                    175 KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 234
                                                                                                                                                                         235 GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tangney M., Mitchell W.J.;

"Analysis of a catabolic operon for sucrose transport and metabolism in Clostridium acetbutylicum ATCC 824.";

EMBL; AF205034; AAF35839.1;

InterPro; IPR001127; PTS_EIIA.

InterPro; IPR001359; PTS_EIIA.

InterPro; IPR001359; PTS_EIIA.

InterPro; IPR001354; Trypsin.

Pfam; PF00358; PTS_EIIA.

Pfam; PF00378; PTS_EIIA.

Pfam; PF00378; PTS_EIIA.

Pfam; PF00378; PTS_EIIA.

Pfam; PF00378; PTS_EIIC.
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                                                                                                                                                                                        Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                                   407 AGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLL
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PROSITE; PS00371; PTS_EIIA_1; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
SEQUENCE 627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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STRAIN-ATCC 824;
MEDLINE-20391269; Pubmed-10937490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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01-OCT-2000 (
01-JUN-2001 (
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Matches
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RESULT Q9L8G6

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SPIVITGLHQSFPPIELELFNQGG---SFIFATASMANIAQGAACLAVFFLAKSEKLKGL 179
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Nucleic Acids Res. 28.4317-4331(2000).
EMBL. APO01508; BAB04015.1;
InterPro; IPR001197; PTS_EIIA.
InterPro; IPR0011996; PTS_EIIB.
Fine Pro; IPR00358; PTS_EIIE.
Pfam; PF00358; PTS_EIIB. 1.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.,
"Complete genome sequence of the alkaliphilic bacterium Bacillus
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PTS_SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT
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Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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Probom; PP002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA 1.1 .
PROSITE; PS01035; PTS_EIIB_CYS; 1.
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584 KEKAVSPIVLTIVTNHEDMGFVNS 607
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In Replace Acids Res. 28:4317-4331(2000).

In Nucleic Acids Res. 28:4317-4331(2000).

In Replace Sequence comparison with Bacillus subtilis.";

In Replace BaB06314 1;

In InterPro; IPR001995; PTS_EIIA.

In InterPro; IPR00352; PTS_EIIA.

In Promo; PF00358; PTS_EIIE.

In Promo; PF00358; PTS_EIIB; 1.

In Promo; PF00378; PTS_EIIA; 1.
 RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                               122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                          297
                                                                                                                                                                    471
                                                                                                                                                                                              357
                                                                                                                                                                                                                                           AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                         GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                                                                                                                            SI---DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEA
                                                                                                                                                                   417 IFYPEDGRGFVAFVIALLISFVLA----AVLTYIVGFKDPVDDEDTLSNESGSENEVKR
                                                                                                                                                                                              EAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGOLVSPVSGKIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      636;
                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT
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                                                                                                                                                                                                                                                                                        AIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
                                                                                                                                                                                                                                                                                                      28.5%; Score 673.5; DB 2; 34.0%; Pred. No. 1.8e-30; Live 78; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                            636 AA
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STRIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans.
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Best Local Simi
Matches 163;
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----GLDVAQAGYQGTVLPVLV 47

2 AMVFPSLVNGYDVAATMAAGEMPMWSLF------

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STRAIN=EL TOR N16961 / SEROTYPE 01;

STRAIN=EL TOR N16961 / SEROTYPE 01;

STRAIN=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                        107
                                                                                                                                                                                                                                                               226
                                                                                                                                                                                                                                                                                                                                                           281
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATAAPVPAGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGVAIV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLYYPTLV-----VLTEGE-PLYTLFTGTIFESPVHITFLGIPVILMSYATSVIPILL 234
                                                                                                                                                                                            295 NLSPIIAGAFLGGFWQVFVIFGLHWGLIPIAINNLVVQGSDPVLAMVFAASFAQIGAVAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                           DFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLA
                                                                                                                                                                                                                                                               VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                                                                                                                                                                                                                                                                                                                                        OGYIIGGLGIFGIPSFLHPADGMDAGFWGIVIAVVVAFV · LGFILTYLFGLKSGNASDEQ
                                                                        VSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLY
                                                                                                                                                                                                                                                                                                                                                           KAVALGAAGFLGVVSI - - - - DAPDMVMF - LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'DNA sequence of both chromosomes of the cholera pathogen Vibrio
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
SUCROSE-SPECIFIC IIBC COMPONENT.
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49.3%; Pred. No. 8.4e-30;
tive 46; Mismatches 87;
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Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004395; AAF96554.1;
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Best Local Similarity 49.3
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholerae.";
Nature 406:477-483(2000)
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01-JUN-2001
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434 GLPGFISINPVHAGWLHYFVGMTISFII----AITVTLILSKRKAN

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SEQUENCE FROM N.A.
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T., Hattori M.,
Ogaswara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                          VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                          KGLAGASGVSAVLGITEPAIFGVŅLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF 236
                                                                                                                                                       HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMVFPSIVNGYDVAATMAAGE-MPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
             61 KRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51232 MW; D88607F6E0AF2E84 CRC64;
                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update SUCROSE-SPECIFIC IIBC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus subsp. aureus N315.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.9%; Score 659; DB 2;
48.6%; Pred. No. 8.4e-30;
tive 53; Mismatches 82;
                                                                                                                                                                                                                                                                            480 AA.
                                                                                                                                                                                                          434 PGIISINPQQIGYYIMGMAISFVAAFALTV 463
                                                                                                                                                                                          237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                                                                      099RO0 PRELIMINARY; PRT; 48 099RO0; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequen 01-JUN-2001 (TrEMBLrel. 17, Last annote PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPOSITA OR SA2167.
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EMBL; AP003137; BAB43469.1; -.
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Best Local S
Matches 139
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185 ALVYPNIAASFTVKHPLYTLFQGTLIVSPIXSTFFGIPIIFPASSYLQTVLPIVVAIWAG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 VGGLLFGLVYSPIVITGLHQSFPPIE-LELFNQGGSFIFATASMANIAQGAACLAVFFLA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 GGMGLFAIPSFIDPKNSMILIHFLIAIAMNFVLGFVLTQFIKIPYLYGEPTSTDSDVDDK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                           Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                   Cote C.K., Cvitkovitch D., Bleiweis A.S., Honeyman A.L.;

A novel beta glucoside specific PTS locus from Streptococcus mutat that is not inhibited by glucose.";

Microbiology 146:1555-1563(2000).

R EMBL; AF206272; AAR89975.1;

R InterPro; IPR001375; PTS_EIIA.

R InterPro; IPR00335; PTS_EIIA.

R Pfam; PF00358; PTS_EIIB.

R Pfam; PF00378; PTS_EIIS.1.

R Pfam; PF00378; PTS_EIIS.1.

R Pfam; PF00378; PTS_EIIS.1.

R ProDom; PD00243; PTS_EIIA.1; UNKNOWN.1.

R PROSITE; PS00371; PTS_EIIA.1; UNKNOWN.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 SKIETFFKKIIPDVVKVFFVVPFFTILITVPLSFLVIGPVMSMASDLVGAIFTGIYGFNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGFLGVVSIDAPD----MVMFLVCAVVTFFIAFGAAIAYGL-YLVRRNGSIDPDATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 KSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 PVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
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                                                                          Last sequence update)
Last annotation update)
PERMEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 658.5; DB 2; 33.8%; Pred. No. 1.3e-29;
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                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20340959; PubMed-10878120;
                                                O1-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, BETA-GLUCOSIDE-SPECIFIC EII BGLP.
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                                                                                                                                                                                                           Bacteria; Firmicutes;
                                                                                                                                                                                   Streptococcus mutans.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              NCBI_TaxID=1309;
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Matches 160;
                                                                                                                                                                                                                                                                                                                                           STRAIN=NG8
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Q9KJ80
Q9KJ80;
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OR SPY1815
                                                                                                                                                      STRAIN-SF370
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Q48408;
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Q48408
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                                                                                                                                                                                                                                                                                                                                                   Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezatc S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an MI strain of Streptococcus pyogenes.";

Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; ARD066630, AKK34748.1; -.

Complete proteome.

SEQUENCE 674 AA; 72490 MW; 4BAA26B40E784878 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFG--GPVG-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 -GLLFGLVYSPIVITGLHQSFPPIELELFNQGG---SFIFATASMANIAQGAACLAVFFL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |: :: :: || ||:||||:||||: || || 388 NRHEEREAEISLDAAISAYLGVTEPALFGVNVKYVYPFVAGMIGSGIAGLLSTTFNVQAN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDE 404
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                                                                                                                                                                                            Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKSEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALGAAGFLGVVSIDAPDMVMFLVC----AVVTFFIAFGAAIAYGLYLVRRNGSIDPDATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 APVPAGTTKAEAEAPAEFSNDSTI·IQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDAPVAT-----APHKTWQGTVITLTSPLTGEVKALSEAVDPVFAQGVMGQGALLQPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PTS SYSTEM ENZYME II.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.4%; Score 647.5; DB 2; 34.4%; Pred. No. 5.8e-29;
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                                               ΑA
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                                                                                       Created)
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                                          PRT;
                                                                                                                                                                                                                                                                                                                        STRAIN=SF370;
MEDLINE=21192684; PubMed=11296296;
                                                                                (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.4
Matches 155; Conservative
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID=1314;
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                                                          099x04;
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MEDITER=21192684; PubMed=11296296;
MEDITER=21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                         Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 ETGHAYAITS----SQGAEVLLHIGIDTESMAGDGFESLVAVGQAVKKGDLLGHFDPSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 IQQLIVVTGIHHIFNFLEAQLIANTGKDPFNAYLTAATAAQAGATLAVAVKTKSTKLKGL
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66; Mismatches 202; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        65725 MW; 64F5FE83524DC4DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 632; DB 2;
Pred. No. 3.9e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%;
35.6%;
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Streptococcus pyogenes.
Bacteria; Firmicutes; E
                                                                                                                                                                                                                                                                                                                                                                                                                                           620 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 620 AA;
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SEQUENCE FROM N.A.
STRAIN=P2;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=1314;
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NCBI_TaxID=571;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 TTKAEAE-----APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 S-----IDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLAOMIPPEGIDAT-----ACVLTLVAG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNCTHFNPLKKQGDEV 405
                 Lai X., Davis F.C., Hespell R.B., Ingram L.O.; "Cloning of calloblose phosphoenolpyruvate-dependent phosphotransferase genes: functional expression in recombinant Escherichia coli and identification of a putative binding region for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus plantarum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ILPSSMKNFFTPAICLAVVVPLTFLIIGPVATWLSQLLANGYQLIYQVAPWLAGAAMGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 621;
                                                                                       disaccharides...

Appl. Environ. Microbiol. 63:355-363(1997).

EMBL. U61727, AAB51563.1; -...

EMSE., D6165, 1678...

InterPro: IPR00127; PTS_EIIA...

InterPro: IPR003352; PTS_EIIB...

R Pfam; PF00358; PTS_EIIB...

R Pfam; PF00358; PTS_EIIB...

R Pfam; PF00359; PTS_EIIB...

R Pfam; PF02378; PTS_EIIE...

R ProDom; PD00243; PTS_EIIB; 1...

R ProDom; PS00243; PTS_EIIB; 1...

R PROSITE; PS00371; PTS_EIIA; 1...

R PROSITE; PS00371; PTS_EIIA; 1...

R PROSITE; PS00371; PTS_EIIA...

R PROSITE PS003
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     25.9%; Score 612.5; DB 2; 32.4%; Pred. No. 4.9e-27; ive 89; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 MEDLINE=97176370; PubMed=9023916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-JUN-2001 (TrEMBLrel, 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 154; Conserv
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Q9L461;
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Matches
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Gaps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 FWQVFVIFGVHWTFVPLMMNNIAKMGYDPLLPILSAAVLSQAGAALAVFLKSRDQKMKAL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAG---- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDPDATAAPVPAGTTKAEAEAPAEFS-----NDSTIIQAPLTGEAIALSSVSDAMFASG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 KLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
              Marasco R., Salatiallo I., De Felice M., Sacco M.;

"A physical and functional analysis of the newly identified by Branch of Lactobacillus plantarum.";

FEMS Microbiol. Lett. 186:269-273(2000).

EMBL: AJS50202; CAB71150.1;

InterPro: IPR001197; PTS_EIIA.

InterPro: IPR001396; PTS_EIIB.

InterPro: IPR001395; PTS_EIIB.

Pfam; PF00358; PTS_EIIB.

Pfam; PF00358; PTS_EIIB.

Pfam; PF00378; PTS_EIIB.

Pfam; PF00378; PTS_EIIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          :06
                                                                                                                                                                                                                                                                                                                                                                                                             Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                  ProDom; PD002243; PTS_EITA; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
SEQUENCE 577 AA, 60877 MW; E8C877050103B5FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 607; DB 2; I; Pred. No. 9.2e-27; 81; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 THFNPLKKQGDEVKAGELLCEFDIDAIKAAG 423
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MEDLINE-20263773; PubMed-10802183;
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MEDLINE=98151780; PubMed=9491080;
                                                                                                                                                                                                                                                                                                                                                                                                             25.7%;
32.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.7
Best Local Similarity 32.6
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1523;
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12;

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Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 EFDIDAIKAAGYEVTTPIVVSN 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||: |: || ||:|:|
578 KFDIERIQNAGYSTQVPIIVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 33.5
Matches 148; Conservative
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Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 AA;
                                                [1]
SEQUENCE FROM N.A.
                       NCBI_TaxID=1360;
    Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09KAS1;
                                                                                                                                                                               lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KAS1
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Q9KAS1
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                    "Isolation and characterisation of an aryl-beta-D-glucoside uptake and utilisation system (abg) from the gram-positive ruminal Clostridium species C. longisporum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 KKIIPDMVKTFLVPFATLLVVVPVTFMAIGPISTIAANALGDLTLAIYNFNPTIAGLFIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVSIDAPD------MVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 VSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last amoniation update)
BETA-GLUCOSIDE-SPECIFIC PTS SYSTEM IIABC COMPONENT (EC 2.7.1.69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                        Brown G.D., Thomson J.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L49336; AACO5713.1; -.
HSSP; P20166; 1GPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7D9CD1B17BE9283E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.9%; Score 589.5; DB 2;
llarity 31.2%; Pred. No. 9.8e-26;
Conservative 80; Mismatches 197;
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InterPro: IPR001127; PTS_EIIA.
InterPro: IPR001396; PTS_EIIB.
InterPro: IPR00345; PTS_EIIC.
Pfam; PF00367; PTS_EIIB. 1.
Pfam; PF00378; PTS_EIIB. 1.
ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIB; 1.
PR05ITE; PS00071; PTS_EIIA. 1.
PR05ITE; PS00071; PTS_EIIA. 1.
SEQUENCE 616 AA, 65890 MW; 7D9CD1817BE
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                                                                                     Gen. Genet. 257:213-218(1998)
Brown G.D., Thomson J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                        STRAIN-B6405
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  RRARE REPRETATION OF THE PROPERTY OF THE PROPE
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LVYSPIVITGLHQSFPPIELELFNQG-GSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDATAAPVPAGTTKA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAEAPAEFSNDST---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGL--DVAQAGYQGTVLPVLVVSWILATIEKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 IFSFTSNITLTGEVSGAIKIMIVSAVAVIAGFVVTYLV----GFEDDVIENPIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, TREHALOSE-SPECIFIC ENZYME II, BC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         012030D819163325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.9%; Score 588.5; DB 2; 33.5%; Pred. No. 1.2e-25; iive 76; Mismatches 185;
                                                                                              Genome Res. 0:0-0(2001).

EMBL, AE006376; AAK0558.1; -

InterPro; IPR001343; ABC_transportr.

InterPro; IPR001127; PTS_EIIA.

InterPro; IPR001382; PTS_EIIB.

InterPro; IPR001382; PTS_EIIB.

InterPro; IPR00383; PTS_EIIB.

Pfam; PF00358; PTS_EIIB.

ProDom; PD0047; PTS_EIIB; 1.

ProDom; PD00243; PTS_EIIB; 1.

ProDom; PD0243; PTS_EIIB; 1.

PROSITE; PS00211; APT_EIIB; 1.

PROSITE; PS00211; APT_EIIB; 1.
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Search completed: March 21, 2002, 16:28:26 Job time: 336 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KRLKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSEKLKGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 SLSSAVSAYLGITEPAMFGVNIRYKFPFVCAIISAAIGGAFITVNGVLANSIGVGGLPGI 434
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01514; BAB05951; --
EMBL; PR001596; PTS_EIIB.

InterPro; IPR001996; PTS_EIIB.
                                                                                                                                                                                                                                                                                                                                                                                         1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGV
                                                                                       Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                Length 470;
                                                                                                                                                                                                                                                                                                                               24.1%; Score 569.5; DB 2; Length 42.9%; Pred. No. 9.3e-25; Live 55; Mismatches 93; Indels
                                                                                                                                                                                                                                                                    Complete protecome. Scours AVO AA; 50185 MW; 3CE67B1E9650F5B9 CRC64;
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SEQUENCE 620 AA; 66148 MW; 1AF6872CFDD7C7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE PERMEASE IIABC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 AA
Bacillus/Staphylococcus group; Bacillus
                                        SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
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                                                                                                                                                                                                                        Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIB_CYS; 1.
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                                                                                                                                                                                                                                                                                                                                                            Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                Similarity
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               NCBI_TaxID=86665
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NCBI_TaxID=1314;
                                                                                                                    Horikoshi K.;
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182 ASGVSAVL-GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240 | 1:4:41:1 | 11|11::41 | 1: 1: 1: 1| 1 | 1: 1: 1: 354 AAGISALLAGITEPALYGVTLKFKKPLYAAMISGGLVGAFIGFVNIASYTFVVPSIIGLP 413
                                                                                                                                                          LKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY 122
                                                                                                                                                                                                                                                                             SIDAP----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQVKSGLSTKQT-LYAPWTGEMLFLSEVPDETFSSKLLGEGFAILPSEGEVYAPFDGEVI 520
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                                                                                                                                                                                                                                                                                                                                                             SPIVITGLHQSFPPIELELFNQGGSFIFATASMA-NIAQGAACLAVFFLAKSEKLKGLAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 QYINPSGGANFTNALIAGTATIVLAFSLTWFMG------IDEE---SPKQVSVAADM 461
                                                                                                                        3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 620;
23.9%; Score 564.5; DB 2; 30.8%; Pred. No. 2.5e-24; ive 93; Mismatches 179;
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DFITSKGYSLISPVVVTN 594
                                                             Conservative
                              Best_Local Similarity
Matches 135; Conserv
         Query Match
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Sequence 15, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli

US-08-985-916-15
US-08-700-651-1
US-08-700-651-2
US-08-928-361B-4
US-08-928-361B-4
US-08-928-361B-13
US-08-928-361B-13
US-08-041-886-14
US-08-041-886-14
US-08-074-912-3
US-08-928-361B-1
US-08-938-361B-1

Sequence

ALIGNMENTS

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APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: CHILCASC
STATE: Illinois
COMPOSE: Illinois
COMPOSE: United States of America
ZIP: 6060-6402
COMPOSE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        омьЕR: US/08/920,812
29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/08920812 Patent No. 5763188 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
US-08-920-812-17
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,547
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REGISTRATION NUMBER: 33,54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
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TYPE: nucleic acid
STRANDEDNESS: double
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818
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ORIGINAL SOURCE:
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STATE: Illinois
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Matches 540; Conserv
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APPLICANT: Ohno,
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                 Length 3615;
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            Score 109.6; DB 1;
Pred. No. 2.2e-23;
0; Mismatches 589;
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              Query Match 7.2'
Best Local Similarity 46.3'
Matches 540; Conservative
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE.OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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Pred. No. 2.2e-23;
0; Mismatches 589;
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFRAX: 312/474-6448
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Clinical Isolate EC-24
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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STRANDEDNESS: double
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2435 TATCAACCTGGATAAGCGAACTGATTGCCGGCGGTTATCTCTGGCTTTATCAGGCGGTTC 2376
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                                                                   432 gtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtcatcactggtctgc
                                                                                                                 CTGCATTTGCGGGGGGGGGGGGGGGGTTCTGGCAAATCTTCGTCATGTTCGGACTGC
                                                                                                                                                                 accagtecttecegecaattgagetggagetgtttaaccagggtggateetteatetteg
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                                                                                                                                                                                                  Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                  Borun
                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 109.6; DB 1;
46.3%; Pred. No. 2.2e-23;
tive 0; Mismatches 589;
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CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-24
US-08-921-177-17
                                         Sequence 17, Application US/08921177
Patent No. 5798211
                                                                                                       APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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312/474-0448
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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Matches 540; Conserv
                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   Illinois
                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleio
STRANDEDNESS:
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RESULT 3
US-08-921-177-17/c
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    caacggcatctatg - - - gctaatatcgcccagggtgcggcatgtttggcagtgttcttcc
                                                                                                                  GCGAACGCGATGCGCAGAAAAAGTGGTGGCGGGATCAGCGGCGTTGACGAGTCTGTTTG
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Sequence 17, Application US/08362577C Patent No. 5807673 GENERAL INFORMATION:

RESULT 4 US-08-362-577C-17/c

APPLICANT: Ohno, Tsuneya APPLICANT: Matsuhisa, Akio

APPLICANT:

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2495 TCACACCATTGCTATGTCTGATGGTTATCACACCCGTCACCTTTCTGCTGGTGGGGCCGC 2436
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APPLICANT: Eda, Sojl
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                        Gerstein, Murray &
South Wacker Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
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Pred. No. 2.2e-23;
0; Mismatches 589;
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/362,577C FILING DATE: 27-MAR-1995 CLASSIFICATION: 536 ATTORNEY AGENT INFORMATION: NAME: Rio-Laures, Li-Hsien REGISTRATION NUMBER: 33,547
                                                                               ADDRESSEE: Marshall, O'Toole, Ger STREET: 6300 Sears Tower, 233 Sou CITY: Chicago STATE: 111inois
COUNTRY: United States of America LIP: 60606-6402
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) STRAIN: Clinical Isolate EC-24
US-08-362-577C-17
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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Best Local Similarity 46.39
Matches 540; Conservative
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APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
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Patent No. 5853998
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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STATE: 11
COUNTRY:
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Pred. No. 2.2e-23;
0; Mismatches 589;
                                           Version #1
                                                                                                                                                                                                                                                             19036/32420
                                                                                            FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/ACENT INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PACENTIN RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/920,828 FILING DATE: 29-AUG-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                                                                TELEPHONE: 312/474-6300
TELEFAX: 212/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                      NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2
Best Local Similarity 46.3
Matches 540; Conservative
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US-08-920-828-17
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1955 TCACCGTCTGGGCCAGCGTTATTGGCGTGTCATTGCCATCGGTTGCGCATTTGTCGGTA 1896
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STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                            1895 CGGTGATGCTTCATTTCATCACGCTAAACGTCAGCCAGCGCAGGGTGCCCC
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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NAME: FORman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 06473.0001-00000
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TORNEY/AGENT TWOMPER/AGENT TWOMPER/AGE
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ZIP: 20005-3315
COMPUTER READABLE FORM:
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US-08-673-190A-3/c
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                                                                                                                                                                                                                                                                                                                         Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
.OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                            DB 2;
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APPLICANT: Klein, Kathrin
APPLICANT: Stegmaler, Sabine
ATTLE OF INVENTION: Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.7e-20
                                                                                                                                                                                                                                                                                                                            Score 97.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08673190A
Patent No. 5985668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 gccaattgagctggagctgtt 525
                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Protaminoharter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                            6.4%;
            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                         LENGTH: 465 base pairs
                                                                                                                                                                                                                                                                                                                                                                       Matches 204; Conservative
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                                                                                                             TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                 Similarity
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TELEPHONE:
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                       US-08-673-190A-3
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EP 91 114 300.6

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FILING DATE: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 CGGTGTGGTTTATGAGCATGGTCGAGAAACGGCTGCGCSSCGTTATCCCTGACGCGCTGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.7%; Score 71.6; DB 2; Length 3
Best Local Similarity 53.1%; Pred. No. 2.4e-12;
Matches 152; Conservative 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 atttcggtggtccagtcggcggtctgctcttcggtctggtctactc 468
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
   APPLICANT: DORNER, F.
   APPLICANT: SCHEIFLINGER, F.
   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
   NUMBER OF SEQUENCES: 52
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Foley & Lardher
   STREET: 1800 Diagonal Road, Suite 500
   CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                  33,694
ER: 06473.0001-00000
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APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,46
                                                                                                                                                                                                                                                                                                  Enterobacter species
           ATTORNEY/AGENT INFORMATION:
NAME: FORTHAN. DAVID S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 0647
TELECOMMUNICATION INFORMATION:
TELEFAN: (2021408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
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SOFTWARE: PatentI
                                                                                                                                                                                                                                             linear
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US-08-673-190A-6
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147 ccaccatggctgcgggcgaaatgccaatgtggtccctgtttggtttagatgttgcccaag 206
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: DAS SQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILLE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 ccggttaccagggcaccgtgcttcctgtgctggtggtttcttggattctggcaacgatcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 gcgatgtgctggcacacggtctacagggactttatgatttcggtggtccagtcggcggtc
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                                            NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09103840A Patent No. 6294328
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
                                                                                                                                      TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-103-840A-2/C
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REFERENCE/DOCKET NUMBER: 7638-005
    ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-460A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 687 tcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcggtaccgcagcta 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 tcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgggcgctgcaggtt 806
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                                                                                                                                                                                                                                                                              DB 4; Length 4403765;
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Pred. No. 18;
0; Mismatches 213; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Leitner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827706artis Corporation
STREET: 59 Route 10
                                                                                 TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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Sequence 1, Application US/08471119A

Patent No. 5827706

GENERAL INFORMATION:
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Best Local Similarity 43.7%;
Matches 165; Conservative
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                      PatentIn Ver. 2.1
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COMPUTER READABLE FORM:
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver.
SEQ ID NO 2
LENGTH: 4403765
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29376 CGATACGGCGCTCTGAGCTCGCTGGAGTGGCCGGTTCGTCAGGGTTCGAAGTTGTCGAC 29317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 cgtttcggcgaatgagttcctgggcgccgcgtattggtatggcgatggtgttcccgag 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 46899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reeders, Stephen
APPLICANT: Schneider, Michael
APPLICANT: Glucksmann, Sandra
ITILE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,751 FILING DATE: US-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                       100-8029/CONT/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Tolypocladium niveum STRAIN: ATCC 34921
US-08-471-119A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08460751 Patent No. 5891628 GENERAL INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100
                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEPHONE: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%;
                                                                                                                                                           FILING DATE: 03-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 55.49
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSE: Pennle &
                                                                                                                                                                                                                                    unknown
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-460-751-1/c
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Length 14060;

DB 3;

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295 cactgcagacttcctgatcactccagtgctgacgttgctgctcaccggattccttacatt 354
                                                                                                                                                                                                                                                                                           235 gctggtggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaaggg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 catcgccattggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacaggg 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920 egeegeaacggeageattgatecagatgeaaccgetgetecagtgeetgeaggaacgaee 979
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APPLICANT: Ranum et al.
TITLE OF INVENTION: SCAT GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SCOTUMER PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 32.6; DB 4;
50.9%; Pred. No. 2.5;
Ive 0; Mismatches 34;
                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                    Pred. No. 16;
                                                                                                                                                                                                                  Score 32.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       980 aaagccgaagcagaagcacccgcagaa 1006
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Crawford, Kathryn P.
Madduri, Krishnamurthy
Merlo, Donald J.
Treadway, Patti J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09135994A Patent No. 6280938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09036987A Patent No. 6143526
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                                                                                                                                                                                                                2.1%;
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LENGTH: 14060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  Best Local Similarity 48.9
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 60.9
Matches 53; Conservative
                                                                                                                   CDS
135..13040
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; ORGANISM: Homo sapiens
US-09-135-994-1
                                                                            MOLECULE TYPE: CDNA
                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Baltz,
APPLICANT: Brought
                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-658-136-4
                                                            TOPOLOGY:
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US-09-036-987A-1
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: OIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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              TELEPHONE: (212) 790-9090
TELEX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12912 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENZYME CORPORATION
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Patent No. 6071717
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 88; Conservative
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STATE: MASSACHUSETTS
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                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-460-751-1
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US-08-658-136-4/c
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APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Crawford, Kathryn P
APPLICANT: Maddwil, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                                         NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOW AGROSCIENCES LLC Patent Department
STRRET: 9330 Zionsville Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/09/036,987A
09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEPAX: (317)337-4841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09370700 Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%;
Best Local Similarity 53.5%;
Matches 68; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 14756 CACGGTT 14762
                                                                                                                                                                                                                STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                61 cgtttcggcggcaatgagttcctgggcgccgcgtattggtatggcgatggtgttcccgag 120
                                                                                                                                                                        DB 4; Length 80161;
                                                                                                                                                                    Score 32.6; DB Pred. No. 52; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: March 22, 2002, 09:23:24 Job time: 8468 sec
                                                                                           ORGANISM: Saccharopolyspora spinosa US-09-370-700-1
                                                                                                                                                                        2.1%;
                                                                                                                                                                    Query Match
Best Local Similarity 53.5'
Matches 68; Conservative
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2
SEQ ID NO 1
LENGTH: 80161
TYPE: DNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticaee; Hordeum.

E. 1 (Dases 1 to 680)

Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.

EST sequencing and analysis in barley

L Unpublished (2000)

Contact: Michalek W

Institute for Plant Genetics and Crop Plant Research

Corrensstr.3, D-06466 Gatersleben, Germany

Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de

Seq primer: T3 primer for 5'end.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL506562 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY02I24T 5', mRNA sequence.
AL506262 GI:12032477
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/cultivar="Barke"
/db_xref="taxon:4513"
/clone="Hy02124T"
/clone=lib="Hordeum vulgare Barke developing caryopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                       CNS0021D
BF727921
CNS025EN
AW573719
BE998387
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BE721200
CNS03HA0
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AI917973
AW440291
AI499080
BE158004
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BG581619
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BG583630
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BI118076
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ALS06262/c
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
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                                                                                           T03017 FB20C8 Feta
AL193990 Tetraodon
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BE997958 EST429681
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                                                                                                                                                                                         ctcatggcatctgcgccgtt......gttgaaaccttgagtgttcg 1527
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                                                                                                                                                                                                                                                                                               22703874
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                  11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                       summaries
                                                                     nucleic search, using sw model
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T03017
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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em_gss_rod:*
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/note="Vector: plasmid pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting

/tissue\_type="developing caryopsis (3.-15.DAP)" /lab\_host="XLOLR"

EST316674 EST482254 EST430136

AW574083 I BG580528 I BE998413 I

Drosophil

Tetraodon Drosophil Tetraodon

AL065923 AL238306 AL078875 AL243904

BE998413 CNSO06U0 CNSO3CVD CNSO0LXJ CNSO3H6V

BE997958 AW574083 BG580528

468.8 441.8 441.6 441.4 441.4 441.4 400.8 400.8

Score

Result . 9

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AI812147 605087403 BI118076 602867346 AL071370 Drosophil AI318021 SWOVAFCAP BE721200 188296 MA AL244017 Tetraodon

AW173566 3 AI917973 1 AW440291 | AI499080 | BE158004 |

AW516253 A A1564728 A AL196412 A A2982613

wt46c03.x EST391869 EST391888

AI982977

Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

DB DB

Minimum Maximum

Database :

AW980716 IAW980735 IBG581619 IBG581892 IBG582423 IBG583630 IBG58360 IBG5860 IBG560 IBG5860 IBG5860 IBG560 IBG560 IBG560 IBG560 IBG560 IBG560 IBG560 IBG560 IBG560 IBG56

Tetraodon

ALO67821 AW583970 ALO31883 ALO97099 BE727921 AL181976 AW573719 BE998387

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Unpublished
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variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5' and 3'-end until a 50 bp window set to 700 bp.

1 204 c 180 g 133 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Steven, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M.

Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459
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                                                                                                                                                                                                                                                                                                     551 CACGGTGATCCCGGCGCTGGTGATGACCTGGTGCCTGTCATATATCGAACGCTGGGTGGA 492
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/clone_lib="Fetal brain, Stratagene"
/note="Vector: Lambda ZAP II; The FB library (catalog #937201, Stratagene) was constructed by directional cloning and oligo d(T) priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthonorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 681)
1 (bases 1 to 681)
1 Neost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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                                                 gi:279156
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Boune
Bernot, A., Fizames, C., Wincker, P., Brottier, P.,
Sauthi, W. and Welssenbach, J.
                                                                                              Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032709637
Fax: 3032707097
Email: nikki@tally.uchsc.edu.
Nature Genet. 2, 180-185 (1992)
94258200
On Sep 21, 1992 this sequence version replaced
Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45.8; DB 11;
Pred. No. 0.17;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="ATCC (inhost):86662"
/db_xref="GDB:DOS2785E"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Genoscope.
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                            ID : COAG262DD07LP1~end : T7" t 50 others
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Corganism-Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="262H14"
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40.9%; Pred. No. 2.2;
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Drosophila melanogaster
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ESTs from senescent nodules of Medicago truncatula
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
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pGVSN-8B9, mRNA
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Pred. No. 2.7;
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/Lissue_type="N2-fixing root nodules"
/Lissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post incoulation with Sinorhizobium meliloti"
/lab_host="E. coll strain xLOLR"
/lab_host="E. coll strain xLOLR"
/note="Vector: pBluescript SR-; Site_1: ECORI; Site_2:
Xhot; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
incoulation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Giappack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
                                          Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
This Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5115
Fax: 651-649-5058
                                                                                                                                                                                                     Minnesota EST name:MZ52981e
TIGR sequence name:MTCAR37TK
More information is available at.
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-51G2"
                                                                                                                                                                                Email: vance004@maroon.tc.umn.edu
Unpublished (2000)
Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GVN"
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Best Local Similarity 50.2%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                              /tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-: Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
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Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., ESTs from one month old nitrogen-fixing root nodules of Medicago
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                  Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M271936e TIGR sequence name:
MTRAKOSTREM More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                     /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                      /clone="pgvsn-8B9"
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AW574083.1 GI:7238816
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50.28;
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Best Local Similarity 50.2
Matches 102; Conservative
  Fax: 651-649-5058
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BG580528 601 bp mRNA EST 11-APR-2001
EST482254 GVN Medicago truncatula cDNA clone pGVN-57H8 5' end, mRNA
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                                                                                                                                                                                                                                                                                  1306 cgatgaagtcaaagcaggggagctgctgtgtgaattcgatattgatgccattaaggctgc 1365
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                                                                       Gaps
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Length 559;
                                                                       Indels
Score 41.4; DB 10;
Pred. No. 2.7;
0; Mismatches 101;
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WALL WALLER

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/Lissue__rip__sanescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="vector: pBluescript SK +/-; Site_1: BcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-zAP KR vector from Stratagene and packaged using Gigapack III Gold packaging extracts; Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                   Fedorova M., Pierson, B.L., Samac, D.A., Gantt, J.S., Vance, C.P., Town, C.D., Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTs from senescent nodules of Medicago truncatula
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                      Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
HI Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACRI4WA1 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL065923 IG:4944891
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M772391e TIGR sequence name:
WRAF954FK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/db_xref="taxon:3880"
/clone="povSN-9112"
/clone_lib="GVSN"
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                                                                                                                                                                                                       Unpublished (2000)
Contact: Carroll P. Vance
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/cultivar="genotype A17"
/cultivar="genotype A17"
/cultivar="genotype A17"
/cultivar="genotype A17"
/clone="lp="cvN"
/clone="l
                                                                                                                                                                                                                                                                                                                                                                                                 Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M381580e TIGR sequence name:
WTCCT40TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA 9AA CTA 9tg 9AT CC).
                                Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                            truncatula, 2001
Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
Vall Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
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50.2%; Pred. No. 2.7;
ative 0; Mismatches 101;
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- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Oscegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

fillers for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                          Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Ins
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 884)
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/db_xref="texon:1727"
/clone_lib="RPCI-98"
/clone="BACR14N21"
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                                     Drosophila melanogaster
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RESULT 10 CNS03CVD/c

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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  survey sequence PUC-Ori end of clone
                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                    Fisher, C.,
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BACR48E16 of RPCI-98 library from Drosophila melanogaster (fruit lly), genomic survey sequence.
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Tetraodon nigroviridis genome survey sequence PUC-Or1 ena or c1015D07 of library G from Tetraodon nigroviridis, genomic survey
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Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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Roest-Croilius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fishk
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="015b07"
/clone_lib="G"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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1 (bases 1 to 983)
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Best Local Similarity 53.0%;
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                                                                                                                                                               Direct Submission

La Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage:
BP 1919 191006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr
- Web: www.genoscope.cns.fr
- Web: www.genoscope.cns.fr
- Oltaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutory Osocopawa and Aaron Mammosor in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2: cn bw sp, the same strain used for the BDGP's pland BST library by the Strain used for the BDGP's pland by an electrical description of the library by the same strain used for the library by an electrical description of the library by the same strain used for the library by an electrical description of the library by the same strain used for the library by an electrical description of the library by the same strain used for the library by the same strain used the same strain s
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/db_xref="taxon:7227"
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tive 96; Mismatches 147;
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/clone="BACR48E16"
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Direct Submission
Submitted (12.APR-2000) to the EMBL/Genbank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Buteleostei; Neoteleostei; Tetraodontidae; Tetraodontidae; Tetraodon.

1 (bases 1 to 970)

2 (bases 1 to 970)

3 (bases 1 to 970)

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6 (bases 1 to 970)

7 (bases 1 to 970)

8 (bases 1 to 970)

9 (bases 1 to 970)
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                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 970)
cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
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Location/Qualifiers
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/db_xref="taxon:99883"
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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/clone_lib="G"
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All Submitsation

AL Submitsation

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVEYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Meb : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
Drosophila melanogaster genome survey sequence T7 end of BAC: BACR23F02 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL067821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 GCTGCCGTTGTTGGCGCTCCATTGATGCTGCTGCTGCTGCTGCAGGCTGCTTCTGTTG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          765 cactetttaatateaaggeagttgegttgggeegetgeaggtttettggggtgttgtteta 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    705 gectgegetggeegttetteateggtateggtacegeagetateggtggegetttgattg 764
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                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterryota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila. ( pases 1 to 993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIO70146 539 bp mRNA EST 05-JUL-1999 UI-R-Y0-lu-g-12-0-UI.sl UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-lu-g-12-0-UI 3', mRNA sequence.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR25F02"
/note="end:T7"
207 c 186 g 151 t 70 c
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48.4%; Pred. No. 12;
tive 1; Mismatches 110;
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                                                                                                                                                                            fruit fly.
Drosophila melanogaster
                                                                                                                        AL067821.1 GI:4957842
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Matches 104; Conserv
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AI070146.1
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TITLE
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/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="vector: pBluescript Sx +/-; Site_1: EcoRI; Site_2:
xhoi; cDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
collected from 2 month old plants at mid-pod stage. The
cDNA was directionally ligated into the Uni: ZAP XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper Apage and propagated in SOLR cells."
                                                                                                                                                                                                                           Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town
,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from senescent nodules of Medicago truncatula
                                                                                             Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                            Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlauq Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1246 cattggtttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcaggg 1305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M271935e TIGR sequence name:
WTKAKOSTK More information is available at:
http://chrysie.tamu.edu/madicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_rref="taxon:3880"
/clone="gGVSN-8B9"
/clone_lib="GVSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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                                                                    Medicago truncatula
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Carroll P. Vance
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Matches 101; Conservative
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CNS00L0P/C
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AUTHORS
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Gaps

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/dev_stage="adult"
//dev_stage="adult"
//dev_s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Eye library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LIML (info@image.llnl.gov). IMAGE ID=1785384 The following repetitive elements were found in this cDNA sequence: 357-476, >(CAA)n#Simple_repeat 478-538, >(CAA)n#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in
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    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                  1 (bases 1 to 539)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              whole-eye library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:10116"
/clone="UI-R-Y0-lu-g-12-0-UI"
/clone_lib="UI-R-Y0"
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Search completed: March 22, 2002, 08:11:36 Job time: 5480 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-921-177-17
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US-08-363-255-13 US-09-007-005-17	US-09-244-796-17	US-08-998-416-915	US-08-022-835-5	US-08-388-809-5	US-08-647-714-5	US-08-370-975B-6	US-08-370-975B-1	US-09-422-869-1	US-08-559-524A-1	US-08-749-707-1	US-08-676-967-2	US-08-676-974-2	US-09-098-487-2	US-08-916-917-1	US-08-972-631-1	US-08-972-629-1
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## ALIGNMENTS

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APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhlaa, Akio
APPLICANT: Watsuhlaa, Akio
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
CORRESPONDENCE 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: united States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
; Sequence 17, Application US/08920812; Patent No. 5763188; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: RICLAURES, LI-HSIEN
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1903(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELERX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDENESS: double
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MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
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TELEPHONE:
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                Length 3615;
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                             6.4e-19;
                DB 1;
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            Score 91;
Pred. No. (
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LIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Watsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagri
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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FILING DATE: 29-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
              8.2%;
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                           Similarity 53.7
10; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
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                                                240;
            Query Match
Best Local Si
Matches 240;
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1798 ATCTGTTCACCGATGACGGGAGATTGTGTCGCCTCATTCACGTCGCTGATACCACGTTT 1739
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 8.2%; Score 91; DB 1; Le Best Local Similarity 53.7%; Pred. No. 6.4e-19; Matches 240; Conservative 0; Mismatches 195;
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Patent No. 5798211
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Wehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagn
                                                                                                                                                                                                                                                                                                         ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                  MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                 LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
312/474-6300
312/474-0448
                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                             SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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us-09-604-231-3.rni

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Matsuhisa, Akio
     Ohno, Tsuneya
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STRANDEDNESS:
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                                      APPLICANT:
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53.7%; Pred. No. 6.4e-19;
tive 0; Mismatches 195; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
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US-08-362-577C-17/C
S. Sequence 17, Application US/08362577C
Patent No. 5807673
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                           NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
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Best Local Similarity 53.7<sup>7</sup>
Matches 240; Conservative
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                     APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                    3: Marshall, O'Toole, Gerstein, Murray 6 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
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27-MAR-1995
11: 536
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                                                                                                                                                                                                               STATE: Illiñois
COUNTRY: United States of America
ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFRERUCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-648
Uehara, Hirotsugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 36.15 base pairs
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
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                                                                           NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
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970 attgttgtttcgaattacaagaaaaccggacctgtaaacacttacggtttgggcgaaatt 1029
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                          790 aaggetgaggatggttecaatgtggatatettgatgeacattggtttegaeacagtaaae 849
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                                                                                                                      850 ctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtcaaagcaggggag
                                                                                                                                                                                                                                                              1510 CGGCTGATTTCTTTTGATATCCCTGCTATTCGCGAGGCCGGATTTGATCTGACGACGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUNRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner STREET: 1300 I Street, N.W., Suite 700 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,190A FILING DATE: 27-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.6%; Score 39.8; DB 2;
62.6%; Pred. No. 0.0048;
tive 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
TITLE OF INVENTION: Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06473.0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                        1030 gaagcgggagccaacctgctcaacgtc 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1390 AGCGCAGGTGAACCGCTGTTATCCATC 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Protaminobacter rubrum US-08-673-190A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08673190A Patent No. 5985668 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Forman, David S.
REGISTATION UNDRER: 33,694
REFERENCE/DOCKET UNDRER: 0647:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)408-400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 465 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 62.69
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-673-190A-3/c
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1738 GCCAGTGGCCTGTTGGGTAAAGGTATTGCCATTCTGCCCTCGGTTGGTGAAGTGCGTTCT 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198 ATCTGTTCACCGATGACGGAGAGATGTGTGCCCTCATTCACGTCGCTGATACCACGTTT 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1678 CCGGTTGCGGGTCGAATTGCTTCGTTGTTCGCCACATTACA-----CGCCATTGGCATT 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 atccaggcacctttgaccggtgaagctattgcactgagcagcgtcagcgatgccatgttt 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 gecageggaaagettggetegggegttgeeategteecaaceaaggggeagttagtttet 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 ccggtgagtgaaagattgtggtggcattcccatctggccatgctttcgcagttcgcacc 789
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                                                                                                                                                                                                                                                                                                                                                                           Probe for Diagnosing Infectious Disease
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                                                                                                                                                                                                                                                                                 APPLICANT: Ohno, Tsuneya
APPLICANT: Matsubisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disea
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ADDRESSE: ANDRESSEE: AMESHAll, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.2%; Score 91; DB 2; Length 361
Best Local Similarity 53.7%; Pred. No. 6.4e-19;
Matches 240; Conservative 0; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: TBM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NATE: US/08/920,828
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 19036/32420 TELECOMMUNICATION INFORMATION:
                                              1030 gaagegggagecaacetgeteaaegte 1056
                                                                                         1390 AGCGCAGGTGAACCGCTGTTATCCATC 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLIÇATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
                                                                                                                                                                                                           Sequence 17, Application US/08920828 Patent No. 5853998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
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INFORMATION FOR SEQ ID NO: 17:
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ATTORNEY/AGENT INFORMATION:
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312/474-0448
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STRANDEDNESS: double
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MOLECULE TYPE: G
ORIGINAL SOURCE:
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                                                                                                                                                               RESULT 5
US-08-920-828-17/c
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LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 acggagectgegatetteggtgtgaacettegeetggegetggeegttetteateggtate 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 ggtaccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttgcgttg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 ggcgctgcaggtttcttgggtgttttttttttgattgctccagatatggtcatgttcttg 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                              69 tctgcaccagtccttcccgccaattgagctggagctgtt 107
                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LATGHER
                                                            99 CATTCACCACACCTCCACGCCGTAGAGGGGGGGCCTGCT
                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDLUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: DEN PC COMPUTER: DEN PC COMPUTER: DOS OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                       Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-232-463-14
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IMMEDIATE SOURCE:
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Db 3923279 TTACCGCCGTCGCCGCCGTTGCCCCCGTCGCCGGATGCCCTGGCTGCCAGCGTTACCG 3923220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3923099 CCGACGGTGCCGTGGGCCCGTTACCGCCGTCACCGCCGTTGCCGCCGTTGCCGCCGTTG 3923040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                  209 tcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagcctgcga 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 tetteggtgtgaacettegeetgegetggeegttetteateggtateggtacegeageta 328
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: PERSER, Claire M. APPLICANT: VENTER, Oldn C. TITLE OF INVENTION: DAS SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                 Length 4403765;
                                                                                                           496 ttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcct 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09135994A Patent No. 6280938
                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4%;
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Best Local Similarity 43.77
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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509 acggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaacgaccaaagccg 568
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                                                                                                                                                                                                             Query Match 2.9%; Score 32.4; DB 4; Length 292; Best Local Similarity 58.2%; Pred. No. 0.85; Matches 57; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)683-4109
                                                                    /product= "sAFP8 (S6)"
/note= "skin-type antifreeze
polypeptide 8 (sAFP8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                     569 aagcagaagcacccgcagaatttcaaacgattccacc 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVALION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; Score 32.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
                      NAME/KEY: CDS
LOCATION: 36.200
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                         US-09-117-121-29
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Fatent No. 6307020
GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION:
ITILE OF INVENTION: Intracellular Antifreeze Polypeptides
ITILE OF INVENTION: and Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARET: California
                                                                                                                                                                                                                                                                                                                                                                                                       Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: CALILOIDING
COUNTRY: CALILOIDING
ZIP: 94111-3834
COMPUTER READBLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-NOV-1998
FILING DATE: 30-NOV-1998
TILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/POCKET NUMBER: 31,677
                 APPLICANT: Ranum et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER APPLICATION NUMBER: 60/056,170
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO: LENGTH: 477
                                                                                                                                                                                                                                                                                                                                                                                                Score 32.6; DB
Pred. No. 0.98;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 aaagccgaagcagaagcacccgcagaa 588
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TELEFAX: (415) 576-0300
INPERATION FOR SEC ID NO: 29.
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.99
Best Local Similarity 60.99
Matches 53; Conservative
                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-09-135-994-1
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GENERAL INFORMATION:
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MOLECULE TYPE:
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                                                                                                                              gacacagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtc 897
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Best Local Similarity 2.2%; Pred. No. 6.6;
Matches 7; Conservative 177; Mismatches 135; Indels
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VENTION: No. 6187580el Pectate Lyases
NCE: 5378.200-US
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48.9%; Pred. No. 2.4;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/198,955A
CURRENT FILING DATE: 1998-11-24
PRIOR PAPLICATION NUMBER: 1343/97
PRIOR FILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/067,249
PRIOR APPLICATION NUMBER: 60/067,249
PRIOR PILING DATE: 1997-12-02
PRIOR PAPLICATION NUMBER: 60/067,240
PRIOR FILING DATE: 1997-12-02
PRIOR PILING DATE: 1997-12-02
PRIOR PAPLICATION NUMBER: 60/067,240
PRIOR FILING DATE: 1997-12-02
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Glad, Sanne O. S.
Kauppinen, Markus S.
Schnorr, Kirk
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Schulein, Martin
Lange, Niels E.
Bjornvad, Mads E.
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; ORGANISM: Bacillus sp.
US-09-198-955A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-198-955A-9/C
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Gaps

90; Indels

Best Local Similarity 48.9 Matches 86; Conservative

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369 tgcgttgggcgctgcaggtttcttgggtgttgtttctattgatgctccagatatggtcat 428

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YASUHIKO YOSHIHARA, AND TSUYOSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3076 GCTAGTCCTGCTGGGTAGGTAGTCTCGTGTATACTGTCTAAAGTTATTCGAAATCAGGT 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 acgattccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtca 655
429 gttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgcagcgattgcttatgg 488
                                  703 CGCCAAAGCGTATGGAAGGTACACGTGAATTGAGGTTTTCAAAGTAGTTATTGTGGAATG 644
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                                                                                                  643 TGATTTTCGGTTGTACGAATCGGAATCAGAAGATCCCATCAGCATGCTCTTCCAG 588
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                                                                           489 cctttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccag
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                                                                                                                                                                                                                                                                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTAD
55 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                          APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, Y. TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB Pred. No. 5; 0; Mismatches
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FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             Sequence 15, Application US/08985916 Patent No. 6221636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 24,616
TELECOMMUNICATION INFORMATION:
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48.98;
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Best Local Similarity 48.99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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321..3077
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           1755
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; LOCATION:
US-08-985-916-15
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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US-08-985-916-15
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTING PARTICLATION NUMBER: US/O8/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 1995-04-03
SOFTWARE: PALING DATE: 1995-04-03
SOFTWARE: PALING DATE: 1995-04-03
SOFTWARE: PALING DATE: 2.0
SOFTWARE: PALING DATE: 2.0
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VERWION: PREPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
VENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
VERWION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
VENTION: SPECIES INFECTIONS
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3136 GGGAATAAGGTTCACCTGGGTTCTCAAACGGCAAAGGAACATTTTCCACATGGCAT 3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 5163;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.9%; Score 32; DB Best Local Similarity 53.1%; Pred. No. 6.3; Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                  Sequence 1, Application US/08700651B
Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-928-361B-4/c
; Sequence 4, Application US/08928361B
; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
US-08-700-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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MEDIUM TYPE: Floppy
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APPLICANT: Petersen, ITILE OF INVENTION: PITILE OF INVENTION: PITILE OF INVENTION: FITILE OF INVENTION: SINUMBER OF SQUENCES:
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STATE: CA
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Pred. No. 6.3;
0; Mismatches
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
RESERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)

US-08-928-361B-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 53.19
Matches 68; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	C.glutamicum phosp C.glutamicum codin C.glutamicum codin C.glutamicum codin Brevibacterium lac Enterococcus faeca S.epidermidis gen Streptococcus pneu Eschtococcus pneu Streptococcus pneu Staphylococcus aur
SUMMARIES	AAF31529 AAF31529 AAF31528 AAF3543 AAF32543 AAX12968 AAV52334 AAV525752 AAV52163
DB	22 22 22 22 22 22 22 23 24 19 19
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## ALIGNMENTS

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers 2elder O, Haberhauer G; Phosphoenolpyruvate; sugar phosphotransferase system; PTS; ds. C.glutamicum phosphoenolpyruvate DNA #2. Schroeder H, BP. 99US-0142691.. 99US-0150310. 99DE-1042095. 99DE-1042097. AAF31529 standard; DNA; 1109 27-JUN-2000; 2000WO-IB00973 Corynebacterium glutamicum. 09-APR-2001 (first entry) Pompejus M, Kroeger B, WPI; 2001-080989/09 (BADI ) BASF AG. WO200102583-A2 01-JUL-1999; 23-AUG-1999; 03-SEP-1999; 03-SEP-1999; 11-JAN-2001 AAF31529; AAF31529 

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                                    The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome,
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation
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Sequence 1527 BP; 304 A; 392 C; 430 G; 401 T; 0 other;

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Score 1107.4;
Pred. No. 0;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lyshne. The present sequence is a nucleic acid described in the exemplification of the invention.
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                                                                                                                                                                                                                                                     amino acid synthesis; vitamin; saccharide;
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Ozaki A;
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Ikeda M,
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988
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Matches 1108; Conservative
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Senoh A,
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Tateishi )
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AAH67869 standard; DNA; 1983 BP.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Senoh A, Ikeda M, Ozaki A;
                                                                                                      amino acid synthesis; vitamin; saccharide; s; ds.
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                                                            C glutamicum coding sequence fragment SEQ ID NO: 2904.
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Pred. No. 0;
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99.9%;
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07-APR-2000; 2000JP-0159162.
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Tateishi N,
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The present sequence encodes the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II. which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
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II obtained by cassette ligation-mediated amplification of downstream
domain of coryneform bacterium sucrase gene, with sucrose-binding
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                                               Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system; ds
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llarity 96.7%; Pred. No. 8.7e-314;
Conservative 0; Mismatches 37; II
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PTS
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  Brevibacterium lactofermentum sucrose
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Best Local Similarity
Matches 1072; Conserv
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Pred. No. 5.2e-29;
0; Mismatches 479; Indels 24;
                                                                                                                                                                                                                                                                                                        use in vaccines for prevention or attenuation of Enterococcus
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                                                                                                                                                                                                                                                                        Enterococcus faecalis relop products for the
                                                                                                                                                                                               CA;
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                                                                                     97US-0066009.
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97US-0046655.
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Best Local Similarity 48.3%;
Matches 470; Conservative (
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                                                                                                                                                                                               Dillon PJ,
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06-MAY-1997;
16-MAY-1997;
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                                        ttcgccgcaacggcattgatccagatgcaaccgctgctccagtgcctgcaggaacga
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used to produce the secondariant present them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing only to SEQ ID NO:4465 to 4472, though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 2913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 120...
59.0%; Pred. No. 1.7e-27;
.*ive 0; Mismatches 163; Indels
.*ive 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2913 BP; 1072 A; 480 C; 419 G; 942 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no sequences are present for SEQ ID NO:4455 to 4464.
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Matches 256; Conservative
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recorded on it, or a representative fragment or a sequence at least 95% identical to SEO ID NO: 1 to 391. The nucleotide sequences depicted in SEO ID NO: 1 to 391 (AAV5224) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEO ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime computer readable medium; vaccine; pharmaceutical composition; ds. Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus pharmaceutical compositions and vaccines for S. pneumoniae Fannon Sequence 3895 BP; 1166 A; 869 C; 805 G; 1055 T; 0 other; Dougherty BA, Claim 1; Page 1179-1182; 1409pp; English. Dillon PJ, (HUMA-) HUMAN GENOME SCI INC 96US-0029960. 97WO-US19588. Streptococcus pneumoniae Choi GH, Rosen CA; WPI; 1998-272225/24 WO9818931-A2 30-0CT-1997; 31-OCT-1996; 07-MAY-1998 Barash SC, Kunsch CA, NAMES OF COLOR COL

and

Gaps 20 tcggcggtctgctcttcggtctggtctactcaccaatcgtcatcactggtctgcaccagt 79 24; Length 3895; Pred. No. 4.5e-26; 0; Mismatches 477; Indels Score 118.8; DB 19; 10.78; 469; Conservative Local Similarity Query Match Best Loca Matches

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254 ttacggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggta 313

2085 TGATTCGTTTTGATATGGATGTCATTAAGGCTGCAGGTCTGGTGAAAACTCCTGTTA 2026 2667 IGACIGGIICAGCCCIIGCAGGCAIGIIAICCGIIACTIIIAAIGIAACIGCGGCIICIA 2608 2547 CAGGAACTATGCTTGCGATTGTTGTTCCAATGCTC-----TGACTTTCTTCTTCC 2494 2193 AGG------GAGTTGAATTGCTCATCCACATCGGTATGGATACAGTAGGTTTG 2146 2145 ATGGCAAAGGTTTTGAAAGTCTTGTAGTCCAAGGAGATCACGTTACAGTTGGTCAGCAAC 2086 253 TTAATGGGACAGTGACGGTTCTTTCCCTACCAAGCATGCCATCGGCATTGTCTCTGACG 2194 tgggcgctgcaggtttcttggggtgttgtttctattgatgctccagatatggtcatgttct 433 434 tggtgtgtgtgtgttaccttcttcatcgcattcggcgcagcgattgcttatggccttt 493 2373 TCAGCCCACTAACTGGCCAAGTGAAGAATTGAGTCAAGCGACGGATCCTATTTTGCAT 2314 854 acggcacgcactttaacccgctgaagaagcagggcgatgaagtcaaagcaggggagctgc 913 gaacgaccaaagccgaagcagcagcagcagaattttcaaacgattccaccatcatcc 613 tgtgtgaattcgatattgatgccattaaggctgcaggttatgaggtaaccacgccgattg 973 teggtacegeagetateggtggegetttgattgeactetttaatateaaggeagttgegt TTGGTATCGGTGGTTTGCCAGGTATTCTCTCTATTCAACCTCAATACATGCTGCCATTTG acttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgccag 614 aggcacctttgaccggtgaagctattgcactgagcagcgtcagcgatgccatgtttgcca 794 ctgaggatggttccaatgtggatatcttgatgcacattggtttcgacacagtaaacctca tgagtggaaagattgtggtggcattcccatctggccatgctttcgcagttcgcaccaagg goggaaagettggetcgggcgttgccatcgtcccaaccaaggggcagttagtttctccgg P.aeruginosa; E.coll; ds. Probe; S.aureus; S.epidermis; E.faecalis; K.pneumoniae; E.cloacae; clinical sample; Escherichia coli genomic probe EC-24. BP. AAQ55752 standard; DNA; 3615 93WO-JP00936 (first entry) 2025 TCATCACCAA 2016 974 ttgtttcgaa 983 Escherichia coli 07-JUL-1993; 25-SEP-1995 WO9401583-A 20-JAN-1994 AAQ55752; 2607 914 374 464 554 AAQ55752/c 314 734 à ò g δ g δy q ŏ 9 οy 8 δý Q δ g ò g ò q Q g ò g 

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                                                                                                                                                                                The nucleotide sequence of a 3615 bp probe obtained by digestion of secherical coll genomic DNA with the restriction enzyme HindIII.

The probes (AAQ55133-48 and AAQ55752-58) represent other probes derived, by HindIII digestion of the genomes of Staphylococcus aureus, Sepidermis, Enterococcus faecalis, Pseudomonas aeruginosa, E.coli, Klebsiella pneumoniae or Enterobacter Cloacae. The probes can be used to detect their respective microorganisms in clinical samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGTTGCGGGTCGAATTGCTTCGTTCGCCACATTACA-----CGCCATTGGCATT 1625
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                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                          Probe for identifying bacteria causing infectious disease -consists of a DNA fragment obtained by HindIII cleavage of the
                                                                                                                                                                                                                                                                                                                        Length 3615;
                                                                                                                                                                                                                                                                                                                      8.2%; Score 91; DB 15; Length 36 llarity 53.7%; Pred. No. 1.7e-17; Conservative 0; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                   Sequence 3615 BP; 966 A; 962 C; 805 G; 882 T; 0 other;
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                                                             Uehara H;
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                                                                                                                                                           Claim 7; Page 62-64; 100pp; Japanese.
                                                                                                                                    pathogenic bacterial genomic DNA
                                                             Ohno T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV52163 standard; DNA; 9769
92JP-0179719
                         PHARM IND LTD
                                                            Matsuhisa A,
                                                                                   WPI; 1994-035086/04
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Best Local Similarity
Matches 240; Conserv
                        (FUSO ) FUSO
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 07-JUL-1992;
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52524) are genomic fragments from Streptcoccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule sproding a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the collaborative which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification or primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the computer based system for identifying readable medium can be used in a computer-based system for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the present invention can be used in diagnosis kits and assays, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8723 TCATCACAGCTGCTATGACAGCTCAAGGTGCTGCTACTGTTGCGGTTGGTGTTAAAACAA
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S. pneumoniae; genome; diagnosis; assay, vaccine; pharmaceutical composition; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9769 BP; 2918 A; 2141 C; 1792 G; 2916 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%; Score 90.2; DB 19;
46.7%; Pred. No. 5.1e-17;
tive 0; Mismatches 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon PJ, Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 318-324; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0029960.
                                                                                                                                                                                                                                                                                                                                               97WO-US19588
Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                   Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-272225/24.
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Matches 490; Conserv
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                                                                                                                                                                                                                                                                   07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
Kunsch CA,
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EP786519-A2

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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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cggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcg 316
                                                                                                                                                                                                                                     tggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaa 556
                                                                                                                                                                                                                                                                                                                                                                                                             gaaagettggetcgggegttgecategteceaaceaaggggeagttagttteteeggtga 736
                                                                                                                                             GTATCACCATCATCCTGGTACAATGCTTTATGTTGGTAACGGACAACTTCCACAATACC
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                                                        gtaccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgg
                                                                                                                  gegetgeaggtttcttgggtgttgtttctattgatgctccagatatggtcatgttcttgg
                                                                                                                                                                           tgtgtgcagttgttaccttcttcatcgcattcggcgcagcgattgcttatggcctttact
                                                                                                                                                                                                                                                              8378 ACATGTTTGGTTACGAAG---ATGAAGTAGACGCAACTGCAGCTGCAAAACGAGCTGAAG
                                                                                                                                                                                                                                                                                              cgaccaaagccgaagcagaagcacccgcagaatttcaaacgattccaccatcatccagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus contig SEQ ID #1317.
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257
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Staphylococcus aureus.

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regalons of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus in fection. The colypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating champing of the S.aureus DNA sequences contained on the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 attgctttcttcaaggttaaagcaatcgcattaggaactgctggattgccaggatttatt
                                                                                                                                                                                                                                                                              Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.4; DB 18; Length 465; Pred. No. 1.8e-13; 0; Mismatches 146; Indels 1
                                                                                                                                                                                            Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 465 BP; 155 A; 69 C; 88 G; 152 T; 1 other;
                                                                                                                                                                                          Fannon MR,
                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1918; 3271pp; English.
                                                                                                                                                                                          РJ,
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                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                    97EP-0100117
                                                                                                                    96US-0009861
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                                                                                                                                                                                                                                             WPI; 1997-374922/35.
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Matches 175; Conserv
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                                                                                  07-JAN-1997;
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                                                                                                                                                                                                          Rosen CA;
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                                                                                                                                                                                          Barash
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1669 agcacaacaaacactgttcacttcaaagatcttactgaggaagtttactcagtagcaga 1728

cggtgaagctattgcactgagcagcgtcagcgatgccatgtttgccagcggaaagcttgg

1789 tgatggatttgcagtagaacctgcaaatggaaacattgtatctccagtttcaggtactgt 1848

747 tgtggtggcattcccatctggccatgctttcgcagttcgcaccaaggctgaggatggttc gtcaagcatcttcccaacaaaacatgcttttggtattgtgacggaagcagg----caatgtggatatcttgatgcacattggtttcgacacagtaaacctcaacggcacgtt

1849

807

1900 867 1957

687

627

746

tacagttcatgttgctgaaggacaaaaagttgcagcaggagatctccttgtcacagctga

998

cttggatgctatccgtgcagcaggacgtgaaacttcaacagtagttgtcttcacaaatgg 2076

987 caagaaaaccggacctgtaaa 1007

2077 tgatgcaattaaatcagttaa

Escherichia coli protein encoding nucleotide sequence SEQ ID NO:137

(first entry)

21-SEP-2001

AAH81338;

BP.

AAH81338 standard; DNA; 1947

Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antiblotic; gene therapy; diagnosis; bacterial growth inhibition; ds.

Escherichia coli.

WO200148209-A2

05-JUL-2001

19-DEC-2000; 2000WO-US34419.

99US-0173005

23-DEC-1999;

tattgatgccattaaggctgcaggttatgaggtaaccacgccgattgttgtttcgaatta 986

927

us-09-604-231-3.rng

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AAH81338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. AAV5254) are genomic fragments from Streptcoccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the cucleic acid molecule sproduced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening of the sequences in SEQ ID NO:1 to 391, identifying members of the Ilbrary which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating ments derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer CC readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products CC readable medium can be used in a computer-based system for identifying contains and incompanies of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products of the present invention can be used in diagnosis kits and assays, and charmacentian and incompanies and used in diagnosis kits and assays, and contains the present invention can be used in diagnosis kits and assays, and charmacentian can be used in the diagnosis of commercial importance.
                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                        S. pneumoniae; genome; diagnosis; ass
vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                         Fannon
                                                                                           Streptococcus pneumoniae genome fragment SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                                         Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1052-1057; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
AAV52296 standard; DNA; 8494 BP
                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                             (first entry)
                                                                                                                        Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                    Barash SC, Choi GH,
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-272225/24.
                                                                                                                                                                                                W09818931-A2
                                                                                                                                                                                                                                                            30-OCT-1997;
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                                                           23-OCT-1998
                                                                                                                                                                                                                               07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae
                            AAV52296;
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The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation
                                                                                                                                                                                                                                                                                                         Novel nucleic acids encoding proteins required for Escherichia coli proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 180-183; 596pp; English.
                                                                                      Zyskind JW;
(ELIT-) ELITRA PHARM INC.
                                                                                  Forsyth RA, Ohlsen KL,
                                                                                                                                                                         2001-457376/49.
                                                                                                                                                                    WPI; 2001-457376,
P-PSDB; AAG98282
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Gaps

12;

Score 67; DB 19; Length 8494; Pred. No. 7e-10; ); Mismatches 250; Indels 13

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Conservative

239;

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6.08;

Ouery Match Best Local Similarity

cgaagcagaagcaccgcagaattttcaaacgattccaccatcatccaggcacctttgac 626

267

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of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular necorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coll proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491
                                                                                                                                                                                                                                                                                                                                                                                represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
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Sequence 1947 BP; 399 A; 498 C; 568 G; 482 T; 0 other;

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ij
                                                                                                           1508 cgccgattaccggtgatgtcgtggcactggatcaggttcctgacgaagcattcgccagca 1567
                                                                                                                                                                                    1568 aagoggtgggtgacggtgtggcggtgaaaccgacagataaaatcgtcgtatcaccagccg 1627
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                                                                         617 cacctttgaccggtgaagctattgcactgagcagcgtcagcgatgccatgtttgccagcg 676
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                                        12;
 Score 66; DB 22; Length 1947; Pred. No. 6.4e-10;
                                      0; Mismatches 220; Indels
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Score 65.2; DB 20; Pred. No. 2.7e-09; 0; Mismatches 238;

5.9%;

Conservative

Similarity

Query Match Best Local Simi Matches 221;

Length 9797;

Sequence 9797 BP; 2839 A; 2360 C; 1699 G; 2898 T; 1 other;

MAX1293 to AAX13919 represent these nucleotide sequences is accalled general AAX1293 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalls genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalls in samples. They can also be used for progression of disease, and for identifying agents which can be used neother related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalls, or an be used in vaccines to prevent or attenuate an Enterococcus faecals.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus

Kunsch CA;

Dillon PJ,

Barash SC,

WPI; 1999-045171/04.

(HUMA-) HUMAN GENOME SCI INC

97US-0066009. 97US-0046655.

98WO-US08985

04-MAY-1998; 14-NOV-1997; 06-MAY-1997; 16-MAY-1997; computer readable medium has been developed which has recorded

Claim 1; Page 1805-1810; 2084pp; English.

infection

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4931 GGTTTGATTCTTGGTTTCTTCTGGCAAGTCTTAGTTATTTTTGGTTTACATTGGAGCGTT 4872
                                                                                                                                                                 4871 GTGCCATTAGCTATTATGCAAGTGACACAAGAAGGTTCAAGCCAAGTATTAACGGGATCA 4812
                                                                                                                                                                                                                                                                          4811 TTTGCAGCTAGTTTTGCGCAAACAGCGGTTGTTTTAGCGATGTTCTTCAAATTGAAAGAT 4752
                                                                                                                                                                                                                                                                                                                                                                                       4751 AAAAAGTTAAAAAGCTTTGTGTCCGCCAGCAATTATCTCTGGTATTTTTGGTGTAACAGAG 4692
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                                                                                                           85 ccgccaattgagctggagctgtttaaccagggtggatccttcatcttcgcaacgg---ca 141
                                                                                                                                                                                                                      142 tetatggetaatategeeeagggtgeggeatgtttggeagtgttetteetggegaagagt 201
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ggtctgctcttcggtctggtctactcaccaatcgtcatcactggtctgcaccagtccttc 84
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(first entry)

19-MAR-1999

AAX13487;

AAX13487/

Enterococcus faecalis;

Enterococcus faecalis

WO9850555-A2 12-NOV-1998

4572

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yokoi H;
                                                                                                                                                                                                                                                                                          Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO: 3461; 246pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2049 BP; 452 A; 553 C; 518 G; 526 T; 0 other;
                                                                                                                                                                                                                         glutamicum coding sequence fragment SEQ ID NO: 3461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                              AAH68426 standard; DNA; 2049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                        organic acid synthesis; ds
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Tateishi N,
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AAH68426
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Gaps

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1583 653

593 caaacgattccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcg

1523 caggigcaggagccgcigciggcgcigcaaccgccgiggcagciaagccgaagciggccg 1582

533 ccgctgctccagtgcctgcaggaacgaccaaagccgaagcagaagcaccgcagaattt 592

5.3%; Score 59.2; DB 22; 47.4%; Pred. No. 8.4e-08; tive 0; Mismatches 233;

Best Local Similarity 47.4 Matches 221; Conservative

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Query Match

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1763 cagiggcatigcgcittaga-----tagcggagitgaaatccitgiccacgitg 1810
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Search completed: March 22, 2002, 08:55:59 Job time: 4728 sec

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AX127152 AX122988 STRSCRA PDCRAFOPER PPSURFOP AP001508

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AX127152 Sequence
AX127182 Sequence
MX2711 Streptococc
L32093 Pediococcus
AF001508 Bacilus
X69800 S.XJosus S
X69801 S.XJosus S
X69801 S.XJosus S
X69802 Pasteurel
AF269422 Pasteurel
AF269422 Pasteurel
AF269422 Pasteurel
AF269422 Pasteurel
AF007479 Streptoco
AM76768 Vibrio algi
S54245 B.Subtilis Su
AF00751 Bacillus Su
AF00751 Bacillus Su
AF229829 Pseudomon
M8172 Erwinia chr
D37921 Altalophiol
AF229829 Pseudomon
M8172 Erwinia chr
D37921 Altalophiol
AF20627 Streptoco
X80203 B.Subtilis
AF001513 Bacillus
AF00563 Streptoco
M1573 Erwinia chr
D37921 Altalophiol
AF20627 Streptoco
M8721 Altalophiol
AF20627 Screptoco
X80203 B.Subtilis
AF001513 Bacillus
AF005650 Sequence
AR035650 Sequence
AR035650 Sequence
AR035650 Sequence

BSGENR BSUB0020 AF229829 ERWBGPA BACISPO

BSTREPA AP001513 AE006630

2543 292550 12086 136254 2134 3615 3615

AR025193 AR038650 AR068497 ECOBGLO AE000449

SXSCRA LL297015 AE004395 AE006222 AE208422 AX144742 AP003365 SPNEUJ902 VIBSCRAK BSTREAPR BSTR

11007 1084.4 1138.4 1138.6 1138.6 1138.2 1133.2 1120.1 1120.1 1120.4 112

1983 2508 21839 296950 296950 5800 10085 2913 341350 151947 2913 14158 1

	1000 - MAT - 30	73 - OBN - 2001					oacteridae;	steriaceae;			c, O. and Haberhauer, G.	sphoenolpyruvat e:					
ALIGNMENTS			018		amicum.	amicum	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Actinomycetales; Corynebacterineae; Corynebacteriaceae;			Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G.	Orynebacterium glutamicum genes encoding phosphoenolpyruvat e:	sugar phosphotransferase system proteins	3 11-JAN-2001;	AFT (DE)	alifiers	
	24 0011 3C1030xx	Sequence 3 from Patent W00102583.	AX069136 AX069136.1 GI:12579018		Corynebacterium glutamicum.	Corynebacterium glutamicum	Bacteria; Firmicutes	Actinomycetales; Cor	Corynebacterium.	1 (bases 1 to 1109)	Pompejus, M., Kroeger	Orynebacterium gluta	sugar phosphotransfe	Patent: WO 0102583-A 3 11-JAN-2001;	BASF AKTIENGESELLSCHAFT (DE)	Location/Qualifiers	11109
	RESULT 1 AX069136	DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	TITLE		JOURNAL		FEATURES	source

SUMMARIES

AP001509 Bacillus X57401 K.pneumonia

AF309637 AP001509 KPSCRYAB

5270 12989 10371 2343 300750 4621

> 90.2 88.6 86.6 85.8

AE007465 8 AF309637 1 a

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AXU69134 1527 bp DNA
Sequence 1 from Patent WO0102583.
AXU69134
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/db_xref="G1:12579017"
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99.98;
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                                                                         /translation="YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIF
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IGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYETTPIVVSNYKKTGP
VNTYGLGEIEAGANLLNVAKKEAVPATP"
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Pred. No. 1.4e-297;
Mismatches 0;
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                                                                                                                                            303 g
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                                      /codon_start=1
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ilarity 100.0%;
Conservative 0;
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Best Local Similarity
Matches 1109; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhan Orynebacterium glutamicum genes encoding phosphoenolpyruvat sugar phosphotransferase system proteins Patent: WO 0102583-A 1 11-JAN-2001;

BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                             Length 1527;
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Corynebacterium glutamicum
Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales: Corynebacterineae; Corynebacteriaceee;
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/db_xref="taxon:1718"
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agtcggcggtctgcttcggtctggtctactcaccaatcgtc 60
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001 3.049.980"
8 c 90621 g 80391 t
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                                                                                                                                                                      349980)
Zoguchi, H., Ando, S., Hayashi, M., Ochial, K., Shi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Otides
790-A 7068 20-JUN-2001;
YO Co., LTD. (JP)
9080
                                                                                                                                                                                                                                                                                                                                                           9.9%; score 1107.4; DB 6; Length 349980;
9.9%; Pred. No. 6e-297;
ve 0; Mismatches 1; Indels 0; G
                                                                                                                                                   Corynebacterineae; Corynebacteriaceae;
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TTGAGTGTTCG 1527
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Qy 601 tccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtcagcgat 660	QQ	928	ATCACTO
Db 110309 TCCACCATCATCCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCAGCGTCAGCGAT 110250	Qy	121	tectte
Oy 661 gccatgtttgccagcggaaagcttggctcgggcgttgccatcgtcccaaccaa	qa	1018	TCCTTCA
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	ΦΦ	1138	GCTGTTC
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10000	δħ		ccagtgo
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4	qa	1498	TCCACCA
AX122988 LOCUS AX122988 1983 bp DNA PAT 11-MAY-2001 DEFINITION Sequence 2904 from Patent EP1108790.	Qy	661 1558	gccatgt           GCCATGT
ACCESSION AA122908.1 GI:14040476 KEVENDEDIG	Qy	721	ttagttt
	qq	1618	TTAGTT
	Qy	781	gttcgca
	qa	1678	GTTCGC
a so	Qy	841	acagtaa
TITLE Novel polynucleotics. JOHNAN PAFART PA 1102301-2 2004 20-7114-2001.	qa	1738	ACAGTA
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Best Local Similarity 99.9%; Pred. No. 1e-290; Matches 1085; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	qa °		GGCGAAA
Oy 1 tatgatttcggcggtccagtcggcgtctgctcttcggtctggtctactcaccaatcgtc 60	ζ	<b>⊣</b>	acacca 
Db 898 TATGATTCGGTGGTCGGCGGTCTGCTTCGGTCTGGTCTACTCACCAATCGTC 957	<b>q</b> O	1978	ACACCA

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          catcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgtttggca
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1395 GTCAGCGCTTCTTGGTATTACAGAACCTGCTCTTTTTGGGGTGAATTTGAAATATCGTTT 1454
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VERSION
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MALIKLISDIFVPIIPPLAGGGLLMALNNFUTSEGLFGYFSLVQQFPIIKGSSDMIQ
IMSAAPFWFLPILVGISAAKRFGANGFLGASIGMIWVAPGAANIIGLAAAPPISKAAT
IGAYTGFWNIFGLHVTQASYTYQVIPVLVAWULLSILEKFFHKRLPSAVDFTFTPLLS
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PAIETQLISAFQNGTGHGDFIFVTASMANVAQGAATFAIYFLTKDKKMKGLSSSSGVS
ALLGITEPALFGVNLKYRFPFFCALIGSASAAAIAGLLQVVAVSLGSAGFLGFLSIKA
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KAQVTDEVLAAPLAGEAVELISVNDPVFSSEAMGKGIAIKPSGNTVYAPVDGTVQIAF
DTGHAYGIKSDNGAEILIHIGIDTVSMEGKGFEQKVQADQKIKKGDVLGTFDSDKIAE
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                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                        J. Bacteriol. 171, 203-211 (2019).
89123027
Draft entry and computer-readable sequence for [1] kindly provided by H.K.Karamitsu, 22-FEB-1989.
Location/Qualifiers
                                                                                                                                                                                                                    1 (bases 1 to 2508)
Sato,Y., Poy,F., Jacobson,G.R. and Kuramitsu,H.K.
Characterization and sequence analysis of the scrA gene encoding enzyme IIscr of the Streptococcus mutans phosphoenolpyruvate-dependent sucrose phosphotransferase system
J. Bacteriol. 171, 263-271 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             termination signal; putative"
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRSCRA 2508 bp DNA BCT 21-MAR-2000 Streptococcus mutans sucrose-6-phosphate hydrolase (scrB) gene, partial cds; and enzyme scr-II gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
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                                                                                                  M22711.1 GI:153799
enzyme scr-II; phosphoenolpyruvate-dependent sucrose
phosphotransferase system; sucrose-6-phosphate hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<1. .28)
/note="sucrose-6-phosphate hydrolase (sciB)"
/codon_start=1</pre>
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50.4%; Pred. No. 5.8e-35;
iive 0; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Streptococcus mutans"/strain="GS-5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA26970.2"
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223. 2217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pediococcus pentosaceus (strain PPE1.0) DNA; Insertion sequence
IS30 homolog (transposable element Insertion sequence IS30 homolo
kingdom Prokaryotae) DNA; Pediococcus pentosaceus (strain PPE1.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1014 cggtttgggcgaaattgaagcg---ggagccaacctgctcaacgtcgcaaagaaagaagc 1070
                                                                                                                                                                                AGTTGTAGGGGTTTCTCTTGGTTCGGCAGGTTTTCTTGGTTTCCTTTTTTAGGCAAG 1574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            834 tttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1983 TATTGATACAGTATCAATGGAAGGTAAAAGGATTTGAACAAAAAGTTCAAGCAGATCAAAA
                                       357 tatcaaggcagttgcgttgggcgctgcaggtttcttggggtgtttctattgatgctcc
                                                                                                                                                                                                                                                                                           agatatggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          714 ggggcagttagtttctccggtgagtggaaagattgtggtggcattcccatctggccatgc
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gccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgattgcactctttaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gattgcttatggcctttacttggttcgccgcaacggcagcattgatccagatgcaaccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 tgctccagtgcctgcaggaacgaccaaagccgaagcagaagcacccgcagaattttcaaa
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JOURNAL AUTHORS TITLE

FEATURES

REFERENCE

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/gene="agaR"
                                                                                                                      5976. .8177
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                                                                                                                                           Leenhouts,K.J., Bolhúis,A.A., Kok,J.J. and Venema,G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPEl.0
Unpublished
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TRAKALDNRWSLYTLITUNLAIVELEDPFEGAALDIRTKWSBGHFFRWWVVGGTVSS
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KTATFARLGSTIGGGLVGVLVMPAVIFFSAKATSTGDNRGWFIFALIICLIALISAWG
VGGTRRUNDSDIRKNRQDTVCVMEIRFARNDGLMAALAFTFYGYGINILGSLEVY
YFTYIMGRRYSFSILSIINTFLGILATSLAPVLSKKFSRRQYFAGGLVFMLGSLAT
TAGSNLMLVLLAAATMFGFPQQMVFLVVLMVITDSVEXGQLKLGHRDESLALSVRPLIF
TAGSNLMLVLLAAATMFGFPQQMVFLVVLMVITDSVEXGQLKLGHRDESLALSVRPLIF
DNA; Insertion sequence IS3 homolog (transposable element Insertion sequence IS3 homolog, kingdom Prokaryotae) DNA; and Pediococcus pentosaceus (strain PPEI.0) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQEGKGTFAAANHPATVLKAGDIFILPKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM
LSGSLLAQVCYLRQVQNGHTYADLSELXVJHIPNSLINDVLGSLITRELYDLLRWY
PADATNIKVKSTEGNALASYYLOENYSTGCTIMDLCHYLNISSYYLYLEKTHANTSP
QKLLTKLRLEDAKQRLSTSNNSVQSIANWGYKDSFTFSKAFKRYSGASPSYYRKSIG
                                                                     Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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                                                                                                                                                                                                                             On May 25, 1994 this sequence version replaced gi:475106.

Location/Qualifiers
1. 2183 /organism="Pediococcus pentosaceus" /strain="PPE1.0"
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/note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="putative"
complement(2929. .3864)
                                                                                                                                                                                                                                                                                                                                                      487. .510 //note="DR2; putative" //rpt=type=direct 488. .561
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/note="RRI: putative"

/rpt_type=inverted

513. .561

/note="DRI: putative"

/rpt_type=direct

2724. .2760
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/transl_table=11
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3909.
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/gene="rafp"
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Leenhouts, K.J., Bolhur
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3909. .5918
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/gene="rafp"
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                                                                                                                      Pediococcus.
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YFTTHEVDAIGIGSFGPIGVNPHDPKYGYITTTPKPGMGDFDFLGHLKSQFNIPLYWT
TDVWBAAVGBSMIGIAKDVPNSIYWTIGTGYGAGYISQNHFNGRTHFELGHWRLNRL
PGDDFKSNCPYHDICLEGLAAGPAVGKRTGKAGKDIPVDDPWPITTDYIAQACVNLT
VAFRAPKILLINGGYNNQRQLFPWIREKFAAYLNGYEEVPPLDDYIVPAGLGNNSGIAG
GLLLAQAALKNA"
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/product = 11product = 11product = 1product = 1pr
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INSYNFNWQLKAGATFQTPEVLMVYTNKGLNAMSQAYHHLIRERVVRSEFKNQERPIV
VNNWEATFFDFNEAKLKPIVDEAKQLGIEMFVLDDGWFGHRDDDNSSLGDWQVDHRKF
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DLGRQAVRNNIFDQLDQLLKSKQIDYIKWDMNRHLSDIYSVALPPERQGEVYHRYVLG
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LVGLNPKLNYQNIATKAIFGGDELMQLGFYDPVVYQDYTTKVYHFKAVTEN"
                                      TFAAGTLGDGFAIKPSDGRILAPFDATVRQVFTTRHAVGLVGDNGIVLLIHIGLGTVK
LRGTGFISYVEEGGHVQQGDELLEFWDPTIKQAGLDDTVIMTVTNSTEFTWMDWLVKP
QIFLTEEKHAEIVAELERTWRTKFDNTTDQVAEKVVTSLDLATPIAGQVIPLAQVNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGELRYPRVDRGFSGNLPGSTDRTFSRDTLPKBYSTAGEMDYHLPAAIVRHTDGANAL
YLVYQGYRIEAGKPKLSGLPAAFVEDETEAETLTIVLVDQVSQVEFDLQYTIYRDRPV
VTRSVQVCNQGDHAVNLEKVASMQIDFTDRQFETITLPGAHANERHPERGSINYGIQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSLITVDQANRVFHLHNQTLSYIFAVEQGGTLSHLYFGGHVDHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="alpha-galactosidase"
/protein_id="AAA25564.1"
/db_xref="GI:475109"
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complement(10727. .11593)
/gene="scrK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(11673. .13832)
/gene="agaS"
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/gene="agas"
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/db_xref="G1:475110"
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/note="IR?; putative"

/rpt_type=inverted
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/rpt_type=direct
10396. 10442
/note="DR1; putative"
/rpt_type=direct
10397. 10443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
                                                                                                                                                          GQAVKATDNILQLHTKA"
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/codon_start=1
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5976. .8177
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RGTSGPQHQPFMALAEPNTTELAGTVIGCALAWSGNFDSTVEVDQYQHSRLTIGLEPD
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FAVSESKYQHLIEHAHQLGLQMLVLDDGWFVNRNGENGQLGDWFVDPIKFPNGLNPLA
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DHLITTLTNLVQNNQLDYLKWDMNRHLTQVGSTHLPAAQQGELYHRYVCGLYDILTRL
KRACPKLIIENCSAGGGRFDFGMLPYTNQTWISDLTDPVDRATIENGFSYLFPPRIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNHQEVADRVLNAIGKNNIQAAAHCATRLKLVIKDESKIDQQAL
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AMASAPFTFLPILLGFSATKRFGGNPYLGATMGMIMVLPSLVNGYSVATTMAAGKMYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNVFGLHVAQAGYOGQVLPVLGVAFILATLEKFFHKHIKGAFDFTFTPMFAIVITGFL
TFTIVGPVLERTVSDALTNGLVGLYRSTGWIGMGIFGLLXSAIVITGLHGTFPAIETDL
TAMVARTGGSFIFPVASAMAIGQGAATLAIFFAFKSQKQKALTSSAGVSALLGITEPA
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AVISFVVAFIPTFIYAKRTLGDDRDQVKSPAPTSTVINVNDEIISAPVTGASSELKQV
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                                                                                                                                                                  NHITASPNAQNGRITPFETRLQLACIGQLGLELNPRQLAPSEQQLLRGALIKYQQLKS
TFIKAHFYRLPTTRHVVAWLIVTADKRQAICCYLNGLNSRVKTQHPLPLHYLDAELAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDQVFSAEIMGKGAAIVPSSDQVVAPADGVITVTYDSHHAYGIKTTAGAEILIHLGLD
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TTLRHHGTTNLQVTALSSAQLDLPTDQYTALTLSGTHAHEANPSFNRLHPGLQTVRSL
                                                                                                                                                                                                                                                                                                                                     /function="enzyme II of the PTS system, sucrose specific"/note="enzyme IIabc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14879 TCTTTGGTTTATTATATTCTGCAATTGTTATTACTGGTCTCCATCAACTTTCCCAGCAA 14820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14699 GCCAAAAGCAAAAAGCCCTGACTTCTTCAGCCGGGGTCTCAGCGTTACTCGGAATTACGG 14640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 ttgagctggagctgtttaaccag.....ggtggatccttcatcttcgcaacgg
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                                                                                                                                                                                                                   SDSSGNRYTGHQLNTMGIPLKPTNADFTSQLIYLCQN"
complement(13852. 15989)
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Pred. No. 2.5e-27;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVTNVQAGEQLVALTAPAASSVAATTV"
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                                                                                                                                                                                                                                                                                          complement(13852. .15807)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence-experimental
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                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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15993. 15998
/gene="scrB"
15993. 17568
/gene="scrB"
16017. 16022
                                                                                                                                                                                                                                                                   /gene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.5%;
Best Local Similarity 57.9%;
Matches 272; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="scrA"
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. (bases 1 to 21839)
Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"mNGEYKTLANKSFESNVLFFGQEACLPNYTYKGNNVRDSYVIHY
IQEGKGTFAAANHPATVLKAGDIFILPKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSGSLLAQKCYLRQVQNGHIYADLSELYKVLHIPNSLINDVLLGSLIYRLFYDLLRWY
PADATNIKVKSTEQENLAVSYLQENYSTGCTIMDLCHYLNLSRSYLYTLFKTHANTSP
QKLLTKLRLEDAKQRLSTSNNSVQSIANMVGYKDSFTFSKAFKRYSGASPSYYRKSIG
                                                                                                                                                                                                                                               enzyme IIabc; fructokinase;
sucrase.
                                                                                                                                                                                                                                                                                                                Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological
Sciences, Department of Genetics, Kerklaan 30, Haren, The
Netherlands, 9751 NN
On May 26, 1994 this sequence version replaced gi:475962.
14519 CCGCATCAGCCATCGGATTCATTTCGATTGCTTCAAAGTCGATTCCAGCATTCATGCTCA 14460
                                                                                                                                                                           24-MAY-1994
                                    PPSURFOP 21839 bp DNA BCT 24.
P.pentosaceus (PPE1.0) sucrose and raffinose operons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="regulation raffinose-operon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pentosaceus"
                                                                                                                                                                                                                                                       alpha-galactosidase; alpha-glucosidase; insertion element; permease; regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name="terminator 4"
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/product= regulator
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/db_xref="GI:475963"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2929. .3864)
/gene="rafR"
complement(2929. .3762)
/gene="rafR"
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/citation=[1]
complement(3859. .3864)
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/db_xref="taxon:1255"
487. .510
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1. 21839
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/rpt_type=INVERTED
513. .561
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/rpt_type=DIRECT
488. .561
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                                                                                                                                                                                                                                                                                                Pediococcus pentosaceus.
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Leenhouts, K. K.
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/note="IR1"
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                                                                                                                                                                                                                                     GI:493728
                                                                                                                                                                                                                                                                                                                                                       Pediococcus.
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/process_cass_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_sec_range_se
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DDDADVKGTFETNGQYQIIIGPGDVDKVYDALIVKTGLKEVTPDDIKAVAAAGQNKNP
LMDFLKVLSDIFIPIVPALVAGGLLMALNNVLTAEHLFWAKSVVEVYPGLKGIAEMIN
                                                                                                                                                                                                                                                                                                                            QSLGRSIEQRPMMFNQRNRIGDFELDTVVGPRGHSKAVLLTLIDRKSRFLWAYRLKDR
TTATVNEALTKFLTTFNGPVHSFTVDRGTEFSGLVSLESQYGIKTYYCHAYTPADVVV
                                                                                                                                                                                                                                                                                               LNHLRLSWSPGMIAHEFKLATKSIYNWLNQGRIGFSLNDLPEHGVRQRRNVDQRSKYN
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WNVFGLHVAQAGYQGQVLPVLGVAFILATLEKFFHKHIKGAFDFTFTPMFAIVITGFL
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                                                                                                                                                                                                                        /translation="SDAVRTKRSASLKWCLPOTHLLGADLLSSITYSERIKIETFCEL
                                                                                                                                                                                                                                                      GLSNIQMGVRLNRSPSTISYELSRCQPYQAELAQTDAEYKRSQCGRKTKLSDELKQKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="fructose 6-phosphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name="fructokinase"
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/function="enzyme II of the P
                                                                      /product="insertion element"
/protein_id="CAA83666.1"
/db_xref="GI:475966"
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/protein_id="CAA83668.1"
/db_xref="GI:475968"
/db_xref="SWISS-PROT:P43470"
                                                                                                                                                                                                                                                                                                                                                                                            MNALIGIYVVFILKGLVLSTLVLKI"
10396. 10442
/note="DR1"
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/gene="scrA"
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/gene="scrA"
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10681. .10716
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/gene="scrK"
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/transl_table=11
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10397. .10443
                                         /transl_table=11
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       /codon_start=1
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Matches 272;
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TILLLETNIGGLYAKNAMIYLVVFAILY TYMDIFYSFKDYGFWSMLPSLTTDSRERE
KTATFRALGSSTIGGGLVGVLWAPAVEFSARATSTGONRGWFIFALITGLIALISANG
VGLGSTIGGGLVGVUMPAVEFSARATSTGONRGWFIFALITGLIALISANG
VGLGTREVDSDIRKNODTVCWMEIFRALAKNDOLLWAALAYLFYGYGINILGSLEYY
YFTYLMGKPKSFSILSINIFIGALIATSLFPYLSKRFRFGYFAGCLYFWIGGSLEYY
IAGSNLWLVLLAATWEGFPQQWYFLVVLWYTDSVEYGQLKLGHRDESLALSVRFLID
KFGGALSHOVYGQIAIISGWFTGATASTTAAGQLFRKLTWRAFPALMLLIAIGIFSK
QIFTLEBKHAEIVABLERGWTRYFFDNATSTYDGVAEKVYTSLDLATPIAGGVIPLAGVNDF
TFAAGTLGDGFAIRSDGRILAFFDATVROYFTTRRAYGLVGDNGIYLLHGGGTVK
LIRGTGFISYVEGGGHVQQGGBLLEFWDPTIKQAGLDDTVIMTYTNSTFFTMMDWLVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:P43466"
/translation="MQEEHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD
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GSLBGTSRIGMNPFLALVHTTERESGDAV GENLVYSGGHAPFELEKODLDQLHEMVG
INSYNFNWQLKAGAFTGTPEPVLMYTNKGLAAMSQAYHLITERVVRSEFKNDERPIY
VNNWEATFFDFNEAKLKPIVDEAKQLGIEMFVLDDGWFGHRDDDNSSLGDWQVDHRKF
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LYELLERLTTAYPHILFEGCSGGGRFDAGMAYYMPQIWASDNTDAVARLTIQYGTSL
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VQYKQIRPLIQFGEFYRLKSPITSNQAAWMFVSPQQDEAIVMVFNLTSYAQPSLTKTK
LVGLNPKLNYQNIATKAIFGGDELMQLGFYDPVVYQDYTTKVYHFKAVTEN"
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YLVYQGYRIEAGKPKLSGLPAAFVEDETEAETLTIVLVDQVSQVEFDLQYTIYRDRPV
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/function="IS-30 (E.coli) like IS element"
                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="permease"
/function="raffinose transport protein"
/citation=[1]
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/citation=[1]
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/protein_id="CAA83665.1"
/db_xref="GI:475965"
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/standard_name="terminator 3"
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Takami,H., Nakasone,K., Hirama,C., Takaki,Y., Masui,N., Fuji,F.,
Nakamura,Y. and Inoue,A.
An improved physical and genetic map of the genome of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Rehamil, and Horikoshi, K.
Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
14759 CCTCGATGGCCAACATTGGGCAAGGTGCCGCCACTTTAGCTATTTTCTTTGCCACTAAGA 14700
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Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G.,
Takami, H., Hirama, C., Fuji, F. and Masui, N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
Extremophiles 3 (3), 227-233 (1999)
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Bacillus halodurans
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Extremophiles 3 (1), 21-28 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakasone, K., Masui, N., Takaki, Y., Sasaki, R., Maeno, G., Sakiyama, T., Hirama, C., Fuji, F. and Takami, H. Characterization and comparative study of the rrn operons of alkaliphilic Bacillus halodurans C-125 Extremophiles 4 (4), 209-214 (2000)
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Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
                                                                                                                                                                                  Takami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, Y., Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K. Sequencing of three lambda clones from the genome of alkaliphilic
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Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
Genome analysis of facultatively alkalihilic Bacillus halodurans
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Takani,H. and Takaki,Y.

Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
Technology Center, Deep-sea Microorganisms Research Group; 2-15
Natsushinm, Yokosus, Ranagawa 237-0061, Japan
(E-mail:takamih@jamstec.go.jp,
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                                                        (in) Extremophiles in deep-sea environments (Ed.);
  HORIKOSHI, K. TSUJII;
: 249-284; Springer-Verlag (1999)
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Extremophiles 3 (1), 29-34 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 tcgatattgatgccattaaggctgcaggttatgaggtaaccacgccgattgttgtttcga 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                               aaaagctcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcggtaccg
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                                                                                                                                                                                                                                                                  Length 296950
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                                                                                                                                                                                                                                                                  Score 138.2; DB 1;
Pred. No. 3.5e-27;
0; Mismatches 493;
                                                                                                                                                                                                                                                                Query Match 12.5%;
Best Local Similarity 48.0%;
Matches 472; Conservative
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WPFLLLLAS ISFLFVPTSSRSSLIESTKNNYRTKELIVSOVAKVVALVSVIYFLLOIA
DRLIIMBEVRNSMTDWAFGKDYGEFYP PHSIGYDQEENNOGSGLMQTDISLTFSLYPVL
NAAGALYIDAVLY PEBEWLRMATEY SOEHIRSIRVNPNYLQAFPLVDENNKRIAIOEEE
TNRVLLVPEQYKDOKEDIIAY FKEDYAYWATMPEYQAESY SHLQEOTFDIIMLASSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3479. .4120

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/codon_start=1

/transl_table=11

/product="ABC transporter (ATP-binding protein)"

/protein_id="BAB04000.1"

/db_xref="G1:10172894"

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                                                                                                                                                                                                                                           EEIKGTIQTLSQTHTRTVRPLHQFPNYVSPYATYQVEQAGTVTKEQFSATLADLFNHY
LEDYVEELEPLTADDFAVQTEPSHVSTTFDPTFPKTLAWTLWGITGLMLMFYIMRNGK
                                                                                                                                                                                                                                                                                                                                                                                                VESFNLYVEPNEGNLIVDPIIQVLTENNSYPWERDFFRGSVGNDPLKVKLLDONTAKT
YEHYLPLLRDLQLDDNAKHLVTVNEGAQKDISEIQRALTLDTILFVLTATIALFMIVQ
SSHLLFAQHKKRFLLRRLFGHSLFRAYRNVLFWTLATWVVILGIALYRHSGTQYLAIV
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NLDVPLELINGSRTVKQQKKKEVLEKVGLFNKLNKKVHSLSGGGQQRVAIARLLLRPC
DLLLADEPTGSLDMANRNVILDLLCQLNKGGMTIVIVTHDPEVADRCDRVITL"
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TFDGGARLEIMCQSGIDKPDQDDRMGWAHIAFSLGSKEAVNQMTGRLHNDG"
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LETSTALLHPYQDYSLKWFTPNTEVDLGHATLASAIILWELDHISAGQPITFYTKSG
LITASKRGEWIELDFPSEQDYGEWYYPNELIDGLGIQPLYVGRNRFDYLIEIDSEGRL
KELNPNFSLLEQIDTRGIIVTSKSTSTFYDFISRCFPPAVGYWEDPYTGSAHCCLGPY
                                                                                                                                                                                                 /translation="MHAWSAAAYADFAVTIPRIDLLGPDIVLSVLEEAATHHQVNLLR
DVQLLGEGDKIALTTFALLTEKSPFLEAIPLRHGSRLTSEDTRDGDLILSSRRTKEDV
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6023. ,7096
/gene-"BH0284"
6023. ,7096
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3479. 4120
/gene="BH0281"
3479. 4120
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/protein_id="BAB04003.1"
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                                                                                                                                /transl_table=11
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/gene="BH0282"
/note="BH0282
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complement(4740.
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/transi_table=11
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/note="BH0280
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/note="BH0283
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QRIDNNELEKGWACAYVDKQTCYWFHPSPYVEWHCGNAFANDHYIGIERCQSKINGIL
TDEQFGENEEASYWIAALLLKKYQLPVNRETYKLHKMFFDTECPARAWSIHLDNAPTN
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-DEC-1992) E. Wagner, Mikrobielle Genetik,
Universitaet Tuebingen, Auf der Morgenstelle 28, 7400 Tuebingen 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /isolate="cured strain C2a"
/db_xref="taxon:1288"
/clone_lib="sub-genomic in Staphylococcus xylosus mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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complement(132. .137)
983 attacaagaaaaccggacctgtaaacacttacggtttgggcgaaattgaagcgggagcca 1042
                                                                                                                                                                                                           10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            Wagner, E., Gotz, F. and Bruckner, R. Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system
                                                                                                                                                                                                                         S.xylosus scrA gene and unidentified open reading frames x69800
                                                                                                                                                                                                                                                                   membrane protein; scrA gene; sucrose transport protein Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
1 (bases 1 to 2655)
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Mol. Gen. Genet. 241 (1-2), 33-41 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                     20797 TGCTCATTCACGTCATAAAGTAA 20819
                                                                                                     1043 acctgctcaacgtcgcaaagaaa 1065
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                                                                                                                                                                                                                                                                                                Staphylococcus xylosus
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1053. .2495
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1053. .2495
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/gene="scrA"
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995. .1000
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94049686
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AUTHORS
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TITLE
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SOURCE
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                                                                                                                                                                                                                                          İFANAPFTLLPILIGFSAAKRFGGNAYLGAALGMILVHPELMSAYDYPKALEAGKEIP
HWILFGLEINOVGYQOLPMIVAYTIATIEKGEKRYYPTATDLDHLETLSTGF
ITFSPYGPLRPRLGYNLSDGITWLYFFEGGAIGGLIFGGLLYAPTVILOHHHSFTAIETG
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PAMFGYNULKLKYPFIGATVGSGIGSATAFFKVKAIALGTAGTGTF
YGIAATTAFIVAFGYTVALSYKFNIEA"
347 c 347 c 521 g 878 t
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Lucsink,E.J., Marugg,J.D., Kuipers,O.P. and de Vos,W.M.
Characterization of the divergent sacBK and sacAR operons, involved
in sucrose utilization by Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atcactggtctgcaccagtccttcccgccaattgagctggagctgtttaacca-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2133 GCTGCGCTTGCAGCGTTCTTTATTAAAAGAAAATAAAAAATTAAAAAGGCGTAGCCTCT
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gene; sacR gene; sucrose-6-phosphate hydrolase.
Lactococcus lactis.
Lactococcus lactis
Bacteria; Firmicutes; Bacillus/Clostridium grou
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Pred. No. 1.7e-
0; Mismatches
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60.1%;
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2837. 2847
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Matches 429; Conserv
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                                                      -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YIPNAAARSLOGKSLKLIGLVFPTIKNIFYAELIEKIEQALFIRGYKAMLATTEÄDEO
KERDYLALLLSNQVDGIIYGSHNLKAHDYIAIEAPIVAFDRLLTPETTVVSSDNFEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILATKALINSGSKKTAIFTGNDNTNSPTYLRRDGYLLELERNQLKPHIIKIPSGWTLL
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                                                              Direct Submission
Submitted (24-JUN-1997) Luesink E.J., Department of Biophysical
Chemistry, Netherlands Institute for Dairy Research (NIZO), P.O.
Box 20, Ede 6714 BA, THE NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTIKQPINDLAELLVDLIIRKIDGDNIDITYQLPVQLHYGID"
complement(join(1283. .2704,2721. .2725,2737. .2743,
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Bacteriol. 181 (6), 1924-1926 (1999)
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complement(1390, .1396)
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                                                                                                                                                               1. .5800
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Luesink, E.J.
J. Bacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3972 TITGCAATTTTATTTGTTACTAAAACATTAAGACAAAAGCTCTTGCAGCTCCAGCTGGT 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 ttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcaggt 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggtggatccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgt 174
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Pred. No. 7.3e-26;
); Mismatches 415; Indels
      sucrose protein"
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                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettellin, H., Richardson, D., Sermotlaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nlerman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 10264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE004395 10264 bp DNA BCT 31-JUL-2000 Vibrio cholerae chromosome II, section 52 of 93 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTGACCCTGTTTTCTCAAAAGAAATTATGGGAAAAGGTATTGCAATCAAGCCTAAATCT 4496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4332 AATGC------AACAACTCAATACCAACTGAGAAAGTTATTATCGATCCA 4376
                                                                                                                                                                                                                                                                                                                                                  4557 TATGGTATAAAAACAAAAATGGAGGT------GAAGTTCTTTACATATTGGA 4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4665 GTAAAAGCAGGGGATTTACTAGGATCTTTTGATAAAGAAGAAATCAAGAAGAGGGGGATTG 4724
                                                                                                                                                           714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttcgcagttcgcaccaaggctgaggatggttccaatgtggatatcttgatgcacattggt 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4605 ATAGATACTGTTTCAATGAATGGTAATGGATTCATACAAAATGTTAAAGTTGGCCAGAAA 4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaa 894
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                                                                                                                                                                                                                                                                                                                                                                                                 getgetceagtgeetgeaggaacgaccaaagccgaagcagaagcacccgcagaattttea
                                                                                                                                                                                                                                                                                                     aacgattccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gggcagttagtttctccggtgagtggaaagattgtggtggcattcccatctggccatgct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaggtaaccacgccgattgttgtttcgaatt 985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE004395 AE003853
AE004395.1 GI:9658068
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MildTilelagginnvtrilapogovvlalkhpplvpHlpDDvs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPEGYTEHIRDPKVITTQGKWQMLLGAQTLAHQGRLAVYHSDDLLHWHFDKLYGDELG
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RIFTPRDASGISLHGASVDAKLYYMAPASAPFNLEVNVQP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFANAPFVYLPVLLAFSASRKFGGNPFLGAALGMLMVHPDLLNGWGFGSASVSGTVPT
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Submitted (14-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:L14685 PID:289864; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="sucrose operon repressor ScrR, putative"
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/db_xref="GI:9658070"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:M76768 SP:P22825 PID:155262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified by sequence similarity; putative"
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/db_xref="GI:9658071"
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                                                                                                                                                               /organism-"Vibrio cholerae"
                                                                                                                                                                                                                                                                                                                                                        /note="biotype: El Tor"
complement(114. .1553)
/gene="VCA0653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4690. .5661)
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/gene="VCA0653"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656 TATGACTCGGCAGGGTTTGTCGGTGGCGCACTGTTTGGCTTTATCTATGCTCTTTTGTG 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tatgatttcggcggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtc 60
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Pasteurella multocida PM70 section 189 of 204 of the complete
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 ctgcgctggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgattgca
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May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S.
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                                                                                                                                                                                                                                                                                                                                                    Length 10264;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 200; Indels
            by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                    Score 127; DB 1;
Pred. No. 3.5e-24;
                                  /codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAP96561.1"
/db_xref="G1:9658076"
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            /note="identified
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Zhang,Q. and Kapur,V.
Direct Submission
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Best Local Similarity
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                                                                                                                                        /translation="mmaluressmerweigdavvdlipdgoqhylkcpg Gapanvanatarlcgrsaffervgndpfgrewoqtlipdgodhylkcpg Gapanvanatarlcgrsaffervgndpfgrewoqtlidbgvcqhlydpphhfgstvv VDLDBHGERSFTFWVWSROPLQLSDIPSFOWGEWHVCCSIAANDOSBSSTFAAIA OWREWGSYSFPPWYREEVGSELQATVMRAVGLADVVRSSEEBLGFLTGTVSSTE GLQAIADFQIPLVVVTLGAKGALVVTPNSRQIVSGKAVKPIDTTGAGDAFVGGLLYRL SVAQWHNQAILLDAVKWANGCGALATTQKGAMTALFNQAALYAFLE" /gene="VCA0657" /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVILNAMQAQEQGAEVLNYCTVEKAERMGDLMHVTLLDEQTQORFERRSHALVNAAGP
WVKQFLNENAHVSSPYGIRLIQGSHIIVPRIHDEPQAYILQNEDKRIYFVIPYLDDYS
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FSGELYQRFIDYLGEKEFARHAQDIFWRRSKLGLNHDTSVVEEVESYLQQKFHABQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MNARSTRETQDEVLDL11VGGGINGAGIAADATGRGLKVGLYDA
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PFLRPAWMIRAGLFLYDNLGKRTSLPASHKVNLKAGSVTKPEWQIGFEYSDCWVDDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="aerobic glycerol-3-phosphate dehydrogenase"
/protein_id="AAF96558.1"
/db_xref="G1:9658073"
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similarity; putative"
/codon_start=1
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identified by sequence similarity; putative"
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/gene="VCA0659"
complement(9444. .10067)
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complement(7648. .9258)
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/translation-"MPFSLSKVRSFFCHFWTSPMYIFNOGKYKSLHAQOVGELAQIRQ
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DRSVVEIFLNGGEKYWTSRFITADRENALDSSRPLCVSVAELKPILLFP
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WHIFGLEIERVGYQGTVIPVLVASWVLATLEKNLRKVVPSFLDNLITPLFALFITGLL
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                                 complement(4859. .6283)
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YOGPHILKR FERQTALISPRREIGFCPGAEFGGFRRWPHYNTKALEMILQGGYARIK
FGSAK DEANLGALPETWRFCINLGGGTSLINGAVDLIADCTA VTNDSGLMHIA
AAVQRPLVALYGPTSPTYTPPLSEKAVIIRLEGGLIKVRKGKDSBGYHQSLLDIQP
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Submitted (24-OCT-2000) Department of Veterinary Pathobiology University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
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                                                                                 Location/Qualifiers
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                                                                                                                                Length 2913;
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480 c 419 g 942 t
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                                                                                                                             Score 123.2; DB 1;
Pred. No. 3.7e-23;
0; Mismatches 163;
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1. .2011
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Ab_xref="taxon:32630"
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                                                         942
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AX144742
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Best Local Similarity 59.0
Matches 256; Conservative
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Submitted (19-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
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(Joses 1 to 2913)

Taylor, J. David, Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,

Taylor, J. David, Kimmerly, W.J., Rivers, P.R., Torruella-Miller, I.,

Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,

Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2913)
Kimmerly,W.J., Taylor,J.David, Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Alshuller,G., Mamo,L., Shepherd, N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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Staphylococcus epidermidis strain SR1 clone step.1003e09 genomic
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Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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                                       DB 1;
                                   Score 126.6; DB 1;
Pred. No. 4.6e-24;
0; Mismatches 199,
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YROQOGKGTVQTKEEDGKFYBANNRISTARAMTISHKDNDMKYRDITEKVPMSESEVNQ
LLKGKGILENRGKYFLEAQEKYEVNVIYLVSHALVETGNGKSELAKGIKDGKRYYNF
FGIGAFDSSANRSGKSYAEKEQWTSPDKAIIGGAKFIRNEYFENNQLNLYQMRWNPEN
PAQHQYASDIRWADKIAKLOMKSYKQFGIKKDDIRQTYYK"
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IKTLDDAKLLDALNGAIRGRQVIINKFAVELNKDIYTGLLSNMASMVFLLGELNVSDL
SDFLNKVNKGLHVANQASPNAKTTIRSLLGVLKDDDMNRSLTYMLNMLKGMSREE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSKVLYQGYTCFRGLIDDIDLKHPDCAKEYWGRKGRVGIVPLLNNQAYWFITINSKEN NHKYSSFGKPHLQAYFNHYPMEVREILDKQSFTGILLHNIYDLKPLKSFVGRTILLG DAAHATTPNMGGAGQAMEDAIVLVNCFNAYDFEKALQRYDKIRVKHTAKVIKRSRKI GKIAQYFSREFVANRIMKMMPNALAAGQTKFLYKSKEK" complement(2515. .3291)
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IQTCDTCTVEIDGKIERSCSTVIDRPMTVNTVNNDVKDAQKEALDRILEKHMLYCTVC
DYNNGDCEIHNTMDAWGLQHQTYEYKEKPYEKDYGPFYRYDPNQCILCGRCVEACQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKIATOOO"
//translation="MKIATOOO"
GDNVLKKLGNHDLAGTKNAGQILST#MYLDDKDRLLTTVKLKSNTLNYTLPRQTLID
IIKSYVKDDVIFTNHEVTHIDNETDKVTIHFAEQESEAFDLCIGADGIHSKVRQSVNA
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/protein_id="BAB58470.1"
/db_xref="GI:14248082"
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3471.1"
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/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="BAB58467.1"
/db_xref="G1:14248079"
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/protein_id="BAB58468.1"
/db_xref="G1:14248080"
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/protein_id-"BAB58469.1"
/db_xref-"GI:14248081"
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/gene="SAV2307"
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/gene="SAV2308"
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/gene="SAV2309"
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/gene="SAV2306"
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/db_xref="GI:14248083"
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/transl_table=11
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/trans1_table=11
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                             /gene="SAV2305"
35. .988
                                                                                                    /gene="SAV2305"
                                                                                                                                             /note="similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (sites)

Lucoda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Kobayashi,N., Tanaka,T., Sawano,T., Inoue,R.,
Katto,C., Sekinizu,K., Hirakawa,H., Kuhara,S., Goto,S.,
Yabuzaki,J., Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K.,
Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus subsp. aureus Mu50 (sub_species:aureus Mu50,
2274 TATGAATTTGGTGGAGCTATTGGTGACTTATATTTGGTTTATTATATGCGCCAATCGTC 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTACAGGAATGCACCATAGCTTTATTGCAGTTGAAACGACATTAATTGCTGATGCGACT 2155
                                                                                                                                                                                                                                                                                           2034 GCGCGGGTATTTCAGCTTTACTAGGAATTACAGAACCAGCAATGTTTGGTGTCAATCTT 1975
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AP003355 BA000017
AP003355.2 GI:14248078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 cgcctgcgctggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgatt 345
                                                                                                               atcactggtctgcaccagtccttcccgccaattgagctg-----gagctgttt 108
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/strain="Mu50"
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On May 29, 2001 this sequence version replaced gi:13874008
Location/Qualifiers
                                                                                                                                                                                                                                                      109 aaccagggtggatccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2094 GCAGCTTTAGCTGCATTCTTTATCATTAAGCAAAATAAAAATTAAAAGGTGTTGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus group; Staphylococcus.
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Direct Submission
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COMPIEMENT (8884. . .9681)
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complement(8884. .9681)
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Search completed: March 22, 2002, 08:55:40 Job time: 8049 sec

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ilarity 55.9%; Pred. No. 2.1e-22;
Conservative 0; Mismatches 205
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Luesink E.J., Marugg J.D., Kuipers O.P., De Vos W.M.;
"Characterization of the divergent sacBK and sacAR operons, involved in sucrose utilization by Lactococcus lactis.";
J. Bacteriol. 181:1924-1926(1999).
EMBL: 297015; CAR09690.1;
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Lactococcus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENZYME II SUCROSE PROTEIN (EC 2.7.1.69).
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Copyright (c) 1993 - 2000 Compugen Ltd
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    protein search, using sw model

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Ouery Match 36.6%; Score 666; DB 2; Length 650; Best Local Similarity 40.1%; Pred. No. 4.1e-33; Matches 147; Conservative 70; Mismatches 114; Indels 36;

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EMBL; APO01508; BAB04015.1; -
InterPro; IPR001127; PTS_EIRA.

InterPro; IPR001996; PTS_EIRA.

InterPro; IPR00395; PTS_EIRA.

Pfam; PF00358; PTS_EIRA.; I
Pfam; PF00378; PTS_EIRA.; I
Pfam; PF00378; PTS_EIRA.; I
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                                              175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQ------APLTGEAIALSSVSDAMFASG
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT.
BH0296.
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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630 Aa; 66978 MW; 6F0218011686ADD5 CRC64;
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NCBL_TaxID=86665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002243; PTS_BIIA; 1.
PROSITE; PS00371; PTS_BIIA_1; 1.
PROSITE; PS01035; PTS_BIIB_CYS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus halodurans.
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Matches 124; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 EAGANLL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 KVGEKIL 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuji F., Hira
Horikoshi K.;
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120 IKAVALGAAGFLGVVSI---DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
                                   SVAVAPGAPGLLTIPIFYPEDGRGFVAFVIAIIISFVLA----AVLTYIVGFKDPVDDE 456
                                                                                                             177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
                                                                                                                                          237 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 296
                                                                                                                                                                                                                                                          60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, APOOLSO9; BAB043441...

InterPro; IPR001127; PTS_EIIA.

InterPro; IPR001352; PTS_EIIB.

InterPro; IPR003352; PTS_EIIC.

PF00358; PTS_EIIA_1: 1.
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                                                                                                                                                                                                                                                                                                                                                                    297 DEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
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BDLINE-20512582; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=86665;
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36.7%; Pred. No. 4.8e-26;
Live 55; Mismatches 150;
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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Pfam; PF02378; PTS_EIIC; 1.
ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 FNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 NKETVNKDIKVEEVES------VVSPVNGKVVLLKNVPDKTFAEGLIGDGIGVDPE 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD 297
                                                                                                                                                                                                                                                                         r sucrose transport and metabolism 824.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG---SFIFATASMANIAQGAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus mutans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                 Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA_1; UNKNOWN_1.
PROSITE; PS00134; TRYPEIM_HIS; UNKNOWN_1.
SEQUENCE 627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                     Created)
Last sequence update)
Last annotation update)
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Last annotation update)
PERMEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 532.5; DB 2; 34.7%; Pred. No. 6e-25; ive 60; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNT 337
                                                                                                                                                                                                                                                               Tangenty M., Mitchell W.J.;
Tangenty M., Mitchell W.J.;
"Analysis of a catabolic operon for sucrose train Clostridium acetobutylicum ATCC 824.";
J. Mol. Microbiol. Biotechnol. 2:71-80(2000).
EMBL; AF205034; AAF35839.1;
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001127; PTS_EIIB.
InterPro; IPR001354; TTYPsin.
Pfam; PF00358; PTS_EIIA.
Pfam; PF00358; PTS_EIIA.
Pfam; PF00357; PTS_EIIA.
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                                                                                                                                                                                                                                STRAIN-ATCC 824;
MEDLINE-20391269; Pubmed-10937490;
                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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Matches 118; Conserv
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=1488;
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                                                                                                                                                        Clostridium.
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Complete proteome.
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                                                                                                                                                                      59 LAVFFLAKSEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIAL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 FNIKAVALGAAGFLGVVSIDAPDMVMFLVC----AVVTFFIAFGAAIAYGLYLVRRNGSI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 DPDATAAPVPAGTTKAEAEAPAEFSNDSTI-IQAPLTGEAIALSSVSDAMFASGKLGSGV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPL 292
                                                                                                                                                    295 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
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                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PTS SYSTEM ENZYME II.
SPY2097.
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                         235 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
                                                                                               23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.6%; Score 539.5; DB 2; Length 36.6%; Pred. No. 2.5e-25; ive 67; Mismatches 123; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1314;
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Q9L8G6 ID Q9L8G6

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Length 627;

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64F5FE83524DC4DC CRC64;

65725 MW;

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EMBL; AE006608; AAK34540.1;
                           620 AA;
              Complete proteome. SEQUENCE 620 AA;
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                                                         Cote C.K., Cyitkovitch D., Beiweis A.S., Honeyman A.L.;

"A novel beta-glucoside-specific PTS locus from Streptococcus mutans
"That is not inhibited by glucose.";

"Microbiology 146:1555-1563(2000).

"Microbiology 146:1555-1563(2000).

"REMEL, APZ06222, AAR899955.1;

"InterPro: IPR001127; PTS_EIIA.

"InterPro: IPR001127; PTS_EIIA.

"R InterPro: IPR00358; PTS_EIIB.

"R InterPro: PR00367; PTS_EIIB.

"R Ffam; PP00367; PTS_EIIC.

"DR Pfam; PP00378; PTS_EIIC.

"DR Pfam; PP00378; PTS_EIIC.

"DR ProDom; PD002243; PTS_EIIA.]; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                              60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                               358 NIMMRTNENKVRQLSIPAFISALFGVTEPAIYGITLPMRVPFIMTCVSGAISGAYLALFN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 VKMQVMGGMGLFAIPSFIDPKNSMILIHFLIAIAMNFVLGFVLTQFIKIPYLYGEPTSTD 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 IKAVALGAAGFLGVVSIDAPD----MVMFLVCAVVTFFIAFGAAIAYGL-YLVRRNGSID 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                            1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIE-LELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 DPDDGIVVAPTKGEVTLVFPTKHAVGLRT--ENGA--EILIHIGMDTVSLAGKGFKSFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                          28.4%; Score 517; DB 2; Length 644; 35.0%; Pred. No. 5.5e-24;
                                                                                                                                                                                                                                                                                                    65; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II.
SCRA OR SPY1815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                   MEDLINE-20340959; PubMed-10878120;
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MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                  Best Local Similarity 35.09
Matches 126; Conservative
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SEQUENCE FROM N.A.
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NCBI_TaxID=1309;
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                                       STRAIN-NG8;
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and
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                                                                                                                                                                                                              62 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                      Gaps
                                                                                                       3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown G.D., Thomson J.A.;
"Isolation and characterisation of an aryl-beta-D-glucoside uptake e
utilisation system (abg) from the gram-positive ruminal Clostridium
species C. longisporum.";
                                                                                                                                                                                                                                                                                                                                                  122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                      182 VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium longisporum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                      20;
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A Brown G.D., Thomson J.A.;
Brown G.D., Thomson J.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L49336; AAC05713.1;
RSP; P20166; 1GPR.
InterPro; 1PR001127; PTS_EIIA.
R InterPro; 1PR001352; PTS_EIIA.
R InterPro; 1PR003352; PTS_EIIA.
R InterPro; 1PR003352; PTS_EIIB.
R Pfam; PF00358; PTS_EIIB; 1.
R Pfam; PF00378; PTS_EIIB; 1.
R Pfam; PF00378; PTS_EIIB; 1.
R Pfam; PF00378; PTS_EIIB; 1.
R Probom; PD001476; PTS_EIIB; 1.
R Probom; PD001243; PTS_EIIB; 1.
R PROSITE; PS00371; PTS_EIIA_1; UNKNOWN_1.
Length 620;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
27.1%; Score 494; DB 2; L
36.8%; Pred. No. 1.4e-22;
iive 47; Mismatches 149;
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  Query Match 27.1%
Best Local Similarity 36.8%
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Query Match

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66 KSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 125
                                                                  LAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALF 118
                                                                                                                                       ----FLG-----VVSIDAPDMVMFLVCAVVTFFIAF 156
                                  285 YNF-MPIGAGVIMGAFWQVFVIFGVHWTFVPLMMNNIAKMGYDPLLPILSAAVLSQAGAA 343
                                                                                                                                                                                                            157 GAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFS-----NDSTIIQAPLTGE 211
                                                                                                                                                                                                                                                                             212 AIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNV 271
                                                                                                                                                                                                                                                                                                 MEDILINE-97176370; PubMed-9023916;
Lai X., Davis F.C., Hespell R.B., Ingram L.O.;
"Cloning of callobiose phosphoenolpyruvate-dependent
phosphotransferase genes: functional expression in recombinant
Escherichia coll and identification of a putative binding region for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 VGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLA 65
YDFGGPVG-GLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                DF1DE2A2A7B81339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELLOBIOSE-SPECIFIC PTS PERMEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.7%; Score 468; DB 2; Best Local Similarity 33.0%; Pred. No. 5.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Environ. Microbiol. 63:355-363(1997).
EMBL; U61727; AAB51563.1; -.
HSSP; P20166; 1GPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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InterPro; IPRO01996; PTS_EIIB.
InterPro; IPRO01996; PTS_EIIB.
InterPro; IPRO0352; PTS_EIIB.
Pfam; PPO0367; PTS_EIIB.; 1.
Pfam; PPO0378; PTS_EIIB.; 1.
ProDom; PD001476; PTS_EIIB.; 1.
PRODOM; PD002243; PTS_EIIB.; 1.
PROSITE; PS00371; PTS_EIIA.; 1.
PROSITE; PS00371; PTS_EIIA.; 1.
SEQUENCE 621 AA; 65492 MW; DP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                       119 NIKAVALGAAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q48408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ::| | ::: | | SKGYSMGGLGIFALPSYINPEGIDRGFYGNVIAMVAGIVVGFIL------MFVTKLND 449
                                                                                                                                                                                        60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                              120 IKAVALGAAGFLGVVSIDAPD------MVMFLVCAVVTFFIAFGAAIAYGLYLVRRNG 171
                                                                                                                                                                                                                                                                                                                                                     SIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSG 231
                                                                                                                                                                                                                                                                                                                                                                                                    VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 291
                                                                                      Gaps
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                                                                                                                     1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactobacillus plantarum.
Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marasco R., Salatiello I., De Felice M., Sacco M.;
A physical and functional analysis of the newly identified bylgproperator of Lactobacillus plantarum.";
FEMS Microbiol. Lett. 186.269-273(2000).
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001956; PTS_EIIA.
                                                                                    33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 577;
                                              26.4%; Score 480.5; DB 2; Length 31.9%; Pred. No. 9e-22; ive 62; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88; Indels
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Pfam; PF00367; PTS_EINB, 1.
Pfam; PF00378; PTS_EINB; 1.
ProDom; P0002243; PTS_EINA; 1.
PROSITE; PS00371; PTS_EINA_1; 1.
SEQUENCE 577 AA; 60877 MW; E8C877050103B5FC CRC64;
7D9CD1B17BE9283E CRC64;
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Last annotation update)
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STRAIN-B21;
MEDLINE-20263773; PubMed-10802183;
65890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 17,
                                                                 Best Local Similarity 31.9%;
Matches 115; Conservative (
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Best Local Similarity 34.1
Matches 118; Conservative
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616 AA;
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01-OCT-2000 (
01-JUN-2001 (
PERMEASE.
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09L461 09L461;

RESULT **091.461** 

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408 AYTMGA---LGIFSFTSNITLTGEVSGAIKIMIVSAVAVIAGFVVTYLV----GFEDDVI 460
                           179 AAPVPAGTTKAEAEAPAEFSNDST---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIV
                                                     461 ENPIP------DKKFNKQKTNKEIIGSPLEGKVIPLSQVKDAAFSAGVMGKGAAIE
                                                                                 PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ
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Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1314;
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Q9A0X4
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                                                                                                                                     231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
350 RDARQKVLAGSAVSAGIFGVTEPAIYGLNLPLRRPFIFGCVYWPIGGAMVG-FSDSHVST 408
                                                                                             446 ACVLTLVAGLPRSSAEQAAVVVAPASV-ND---ILAPWTGSVLALDQVPDSTFASGLLGQ 501
                                                                                                                                                                                           291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                             558 AHVKEGDKIKAGDLLLEFDRQAILDAGYDLATPIIISNSDDFRTLDMVSASAVDAGQPLL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 FNPIIFGLVLGFAWQVLVMFGLHWAIVPFAIIALAKGEPTALLIAASVASFAQTGAVGAV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQG-GSFIFATASMANIAQGAACLAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                          126 GAAGFLGVVS-----IDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD
                                                                                                                                                     177 ATAAPVPAGTTKAEAE-----APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGS
                                                                                                                                                                                                                                                                                                                                                          QGCKG;
QGCKG;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCCOSIDE-SPECIFIC PTS SYSTEM IIABC COMPONENT (EC 2.7.1.69).
                                                  ----VWGGAAGMFASLII-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       012030D819163325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL. AE006376; AAK0558 1; -.
EMBL. AE006376; AAK0558 1; -.
InterPro; IPR001343; ABC_transportr.
InterPro; IPR001127; PTS_EIIB.
InterPro; IPR001396; PTS_EIIB.
InterPro; IPR001381; PTS_EIIB.
Pfam; PF00376; PTS_EIIB. 1.
Pfam; PF00377; PTS_EIIB. 1.
ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD001478; PTS_EIIB; 1.
ProDom; PD00243; PTS_EIIB; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 448; DB 2;
Pred. No. 9.2e-20;
                                                  409 YSFGFGNIITLAOMIPPEGIDAT------
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33.0%;
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Best Local Similarity 33.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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636 AA;
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618 SVSR 621
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Q9CFK9
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.S., En O., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an Ml strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIIGLPQYINPSGGANFTNALIAGTATIVLAFSLTWFMG-----IDEE---SPKQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMA-NIAQGAACLAVFFLAKSEK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 ILGAIMPLVVMTGMHWAFAPIFLAASVATPDVLILPAMLASNLAQGAASLAVAFKTKQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GFLGVVSIDAP----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66148 MW; 1AF6872CFDD7C7D6 CRC64;
                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE PERMEASE IIABC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%; Score 445.5; DB 2; 33.0%; Pred. No. 1.3e-19; ive 63; Mismatches 131;
                                                                                                                                                                                                                                      AA.
GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
                               620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=SF370;
MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCEFDIDAIKAAGYEVTTPIVVSN 328
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| LLKMDIDFITSKGYSLISPVVVTN 594
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Sest Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAPVPAGTTKAEA--EAPAEFSNDSTIIQAPL----TGEAIALSSVSDAMFASGKLGS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 ----GVPAQEEDQETINHIIAEKGKDKNLRTSSLGNVVEGEVISLNEVKDQAFSTGALGK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 IKAVALGAAGFLGVVS-IDAPDMV--MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Franz C.M.A.P., Worobo R.W., Quadri L.E.N., Schillinger U., Holzapfel W.H., Vederas J.C., Stiles M.E.;
"Atypical genetic locus associated with constitutive production of enterocin B by enterococcus faecium BFE 900.";
Appl. Environ. Microbiol. 65:2170-2178(1999).
EMBL, AF121254; AAD28228.1;
                                                                                                                                                                                                                                              Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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397 VKAYSV-AWGLFGLPAYIGEGDFMNFWFWLMAAVVISFA--GSAVA--AYLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9AECD1C6BF2DEC9C CRC64;
                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE SPECIFIC TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%; Score 433.5; DB 2; 35.1%; Pred. No. 6.9e-19; ive 62; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 AA.
                             618 AA
                                                                                         Created)
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01-JUN-2001 (TrEMBLrel. 17, Created)
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BFE 900;
MEDLINE=99240446; PubMed=10224016;
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PROSTIE; PS00371; PTS_EIIA_1; 1
PROSTIE; PS01035; PTS_EIIB_CXS; SEQUENCE 618 AA, 67051 MW; 6
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InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
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Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
                                                                                            (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.8
Best Local Similarity 35.1
Matches 128; Conservative
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                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1352;
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                                                                                         01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                Enterococcus
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                                                           09X565;
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                             09X565
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Q99RQ0
ID Q99RQ0
AC Q99RQ0
DT 01-JUN
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Q9X565
                                 HODEN TO THE PROPERTY OF THE P
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SERAIN=EL TOR NIG961 / SEROTYPE 01;
STRAIN=EL TOR NIG961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Meldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Uchiyama I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio. NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ALFNIKAVALGAAGFLGVVSIDA--PDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 AA; 51232 MW; D88607F6E0AF2E84 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT.
SCRA OR SA2167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCT-2000 (TrEMBLrel. 15, Created)
OCT-2000 (TrEMBLrel. 15, Last sequence update)
UNN-2001 (TrEMBLrel. 17, Last annotation update)
SYSTEM, SUCROSE-SPECIFIC IIBC COMPONEWT.
                                                                                                                            Staphylococcus aureus subsp. aureus N315.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%; Score 418.5; DB 2;
49.7%; Pred. No. 4.1e-18;
Live 32; Mismatches 47;
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EMBL; AE004395; AAF96554.1; -.
TIGR; VCA0653; -.
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InterPro; IPR003352; PTS_BIIC.
Pfam; PF00367; PTS_BIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).
EMBL, AP003137; BAB43469.1;
Complete proteome.
SEQUENCE 480 AA; 51232 MW
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01-OCT-2000
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1;
                                                                                                                                              57 ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
                                                                                                                      4; Gaps
                                                                                      Ouery Match
22.8%; Score 416; DB 2; Length 479;
Best Local Similarity 52.4%; Pred. No. 5.8e-18;
Matches 86; Conservative 26; Mismatches 48; Indels
Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Complete proteome.
SEQUENCE 479 AA; 50292 MW; DC0E129229957E3C CRC64;
                                                                                                                                                                                                                                                                  117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 160
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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March 21, 2002, 16:28:49 ; Search time 17.08 Seconds
(without alignments)
777.088 Million cell updates/sec US-09-604-231-4 1821 Title: Perfect

1 YDFGGPVGGLLFGLVYSPIV.....IEAGANLLNVAKKEAVPATP 362 score: Sequence:

100059 seqs, 36664827 residues , Gapext 0.5 BLOSUM62 Gapop 10.0 , Searched:

Scoring table:

100059 hits satisfying chosen parameters: Total number of

DB seq length: 0 DB seq length: 200000000 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P12655 streptococc	P43470 pediococcus		P26207 erwinia chr		P51184 staphylococ	09cjz2 pasteurella	P22825 vibrio algi	_	_		_		P08470 salmonella				_	P39816 bacillus su	Q44840 borrelia bu	P50829 bacillus su			P36672 escherichia	P08837 escherichia		P45338 haemophilus				P75569 mycoplasma	P47315 mycoplasma	
SUMMAKIES		PTSA_STRMU	PTSA_PEDPE	PTBA_BACSU	PTBA_ERWCH	PTBA_ECOLI	PTSB_STAXY	PTSB_PASMU	PTSB_VIBAL	PTGA_CORGL	PTTB_BACSU	PTAA_KLEPN	PTSB_BACSU	PTGA_BACSU	PTSB_SALTY	PTAA_ECOLI	PTGA_BACST	PTSB_KLEPN	SACX_BACSU	YBFS_BACSU	PTGA_BORBU	YPQE_BACSU	LACY_STRTR	PTGA_MYCCA	PTTB_ECOLI	PTGA_ECOLI	PTGA_SALTY	PTGA_HAEIN	PTGA_BUCAI	RAFP_PEDPE	LACY_LACDE	PTGA_MYCPN	PTGA_MYCGE	PTDA_ECOLI
	Length DB	664 1			631 1											648 1	324 1	456 1	459 1													940 1		485 1
ar (	Query Match Le	39.0	38.8	28.3	27.0	24.7	24.5	23.0	22.6	21.2	18.1	17.2	16.7	16.4	16.3	16.2	16.2	16.1	15.0	14.9	14.1	14.0	13.9	13.7	13.7	13.5	13.4	13.1	12.7	12.1	12.1	11.4	10.8	9.1
	Score	711	706.5	515	492.5	450	446.5	418	412	386.5	330	313	305	299	296.5	295	294.5	293.5	273	270.5	256	255	252.5	249.5	249.5	246	244	238.5	231.5	221	219.5	208.5	197.5	165.5
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EMBL; M22711; AAA26971.1; -. EMBL; D13175; BAA02466.1; -.

Q9kvd9 vibrio chol Q48624 leuconostoc	P77272 escherichia P39886 streptomyce 003744 bacillus th	Q9ny46 homo sapien P55338 vibrio harv	P15921 ricketts1a Q45400 bacillus st	P24400 lactobacill O9kqh9 vibrio chol	Η.
PTSB_VIBCH LACY_LEULA	YFEV_ECOLI TCMA_STRGA Clan Bacta	CIN3_HUMAN	OMPA_RICRI PTCC_BACST	PTLB_LACCA	OMPB_RICRI
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482 639	474 538 1179	1951	2249	577	1654
8.8 6.9	800	0.0	5.0	5.7	5.6
161.5 157.5	151.5 115.5 113.5	110	107.5	104	101.5
34	37	9 6 4	41	<b>4</b> 4	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;
"Isolation, characterization and sequence analysis of the scrK gene encoding fructokinase of Streptococcus mutans.";
J. Gen. Microbiol. 139:921-927(1993).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                            01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC INABC COMPONENT (EINABC-SCR) (SUCROSE-PERMEASE INABC COMPONENT) (FHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                  Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; "Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans phosphoenolpyruvate-dependent sucrose phosphotransferase system."; J. Bacteriol. 171:263-271(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILD DOMAIN.
                                       664 AA
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                           STRAIN=GS-5;
MEDLINE=89123027; PubMed=2536656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93329360; PubMed=8336109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 639-664 FROM N.A.
                                         STANDARD;
                                                                                                                                                                                                                                   Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Streptococcus.
NCBI_TaxID=1309;
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                                     PTSA_STRMU
P12655;
RESULT 1
PTSA_STRMU
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Best Local Sim
Matches 154;
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MOD_RES
MOD_RES
SEQUENCE
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
17-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 38, Last annotation update)
18-JUL-1999 (Rel. 31, Lel. 32, Lel. 32, Lel. 32, Lel. 33, Lel. 33, Lel. 33, Lel. 33, Lel. 34, Lel. 34, Lel. 35, Lel. 36, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pediococcus pentosaceus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL---FNQG---GSFIFATASMANIAQ
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                                                                                                                                                                                                                                                                                                                                                                                          Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                          116; Indels
                                                                                                                                                                                                   Phosphotransferase system: Sugar transport; Transferase;
Phosphorylation; Transmembrane.
                                                                                                                                                                                                                                                                                                                                         809E63E32281A9A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     39.0%; Score 711; DB 1;
42.1%; Pred. No. 3.8e-43;
tive 73; Mismatches 116.
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                                                                                                                                Probom; PD001476; FTS_EIB; 1.
Probom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA, 1.
PROSITE; PS01035; PTS_EIB_CYS; 1.
              HSSP; P08837; 2F3G.
InterPro; IPR001127; PTS_BIIA.
InterPro; IPR001996; PTS_BIIB.
InterPro; IPR003352; PTS_BIIC.
Pfam; PF00356; PTS_BIIC. 1.
Pfam; PF00356; PTS_BIIB. 1.
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664 AA;
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SEQUENCE FROM N.A.
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P43470;
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57 ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 QVKSPAPTSTV-----INVNDEIISAPVTGASESLKOVNDOVFSAEIMGKGAAIVP
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PHOSPHORYLATION (BY SIMILARITY).
CRSPHORYLATION (BY SIMILARITY).
CRSPA02DOS50A77F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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HSSP; P20166; 1AX3.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001352; PTS_EIIA.
InterPro; IPR003352; PTS_EIIB.
InterPro; IPR003352; PTS_EIIB.
InterPro; IPR00358; PTS_EIIB.
IPR0STTE; PS00311; PTS_EIIB.
IPR0STTE; PS00315; PTS_EIIB.
IPR0STER; PTS_EIIB.
IPR0STER; PS00315; PTS_EIIB.
IPR0STER; PTS_EIIB.
IPR0STER; PTS_EIIB.
IPR0ST
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PHOSPHORYLATION
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Johnson
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-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEBREARE THE PIT THE ISONOMING THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALY TRANSFERS IT TO
                            DEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "New beta-glucoside (bg1) genes in Bacillus subtilis: the bg1P gene product has both transport and regulatory functions similar to those of Bg1F, its Escherichia coli homolog.";

J. Bacteriol. 177:1527-1535(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-168 / BGSC1A1;
MEDLINE-95219088; PubMed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   (EIIABC-BGL)
                                                                                                                                                                                                                                                                                           P40739; Q45661;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-BC (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168;
MEDLINE-96204517; PubMed-8628237;
Beloin C., Hischbein L., le Hegarat F.;
"Suppression of the B91+ phenotype of a delta hns strain of Escherichia coli by a Bacillus subtilis antiterminator binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIA DOWAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
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STRAIN-168 / MARBURG;
MEDLINE-95189730; Pub<u>m</u>ed-7883710;
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                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                649
                                                                                               355 KEAVPAT 361
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                                                                                                                                                643 ASSVAAT
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60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                             Intert.

Pfam: PP00358; ..._

Pfam: PP00379; PTS_EIIB; ...

R Pfam: PF00278; PTS_EIIB; ...

R Probom: PD001476; PTS_EIIB; 1.

DR PROSITE; PS00371; PTS_EIIB, 1.

DR PROSITE; PS01035; PTS_EIIB_1; 1.

DR PROSITE; PS01035; PTS_EIIB_1; 1.

DR PROSITE; PS01035; PTS_EIIB_2; 1.

RW Phosphorylation; Transmembrane; Complete proteome.

And IN 1 1 EIIB DOMAIN.

Propherylation; Transmembrane; Complete proteome.

Propherylat
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Pred. No. 2.6e-29;
3; Mismatches 142; Indels
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POTENTIAL.
POTENTIAL.
A - S (IN REF. 2).
E -> G (IN REF. 2).
E -> G (IN REF. 2).
DG -> HR (IN REF. 2).
I -> M (IN REF. 2).
I -> M (IN REF. 2).
G -> S (IN REF. 2).
W, 5F630C671D21FBED CRC64;
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                                                                                                                                                           Interpro; IPR001127; PTS_EIIA.
Interpro; IPR001996; PTS_EIIB.
Interpro; IPR003352; PTS_EIIC.
Pfam; PF00338; PTS_EIIA_1; 1.
Pfam; PF00367; PTS_EIIB_1; 1.
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33.2%;
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                                     EMBL; X85408; CAA59697.1; EMBL; Z99124; CAB15963.1; PIR; S47174, S47174. HSSP; P20166; LAX3. Subtilist; BG10934; bglP.
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64550
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Best Local Similarity 33.28
Matches 121; Conservative
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PHOSPHORYLATION (BY SIMILARITY).
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MEDLINE=88009877; PubMed=3309161;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92121114; PubMed-1732212;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Control beta-glucoside
utilization in Erwinia chrysanthemi: comparison with the Escherichia
coli bgl operon and evidence for a new beta-glycohydrolase family
including enzymes from eubacteria, archeabacteria, and humans.";
J. Bacteriol. 174:765-777(1992).
J. Bacteriol. 174:765-777(1992).
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
FUNCTION: THIS IS A COMPONEN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HRR): IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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-!- SIMILARITY: CONTAINS A PIS BITA DOMAIN.
-!- SIMILARITY: CONTAINS A PIS BITC DOMAIN.
                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, BETA-GLUGOSIDES-SPECIFIC ITABC COMPONENT (EITABC-BGL)
(BETA-GLUCOSIDES-PERMEASE ITABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (ÉII-BGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON ARBG (BY
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Pfam; PF00.5.,
Pfam; PF00367; PTS_bill;
Probom; PD001476; PTS_EIIC; 1.
A Probom; PD001476; PTS_EIIB; 1.
A PROSITE; PS00371; PTS_EIIB; 1.
DR PROSITE; PS01035; PTS_EIIB, 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
DR PROSITE; PS01036; PTS_EIIB_CYS; 1.
DR PROSPHOFULATION; Transferase;
KW Phosphorylation; Transmembrane; Inner membrane.
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001392; PTS_EIIC.
Pfam; PF00358; PTS_EIIA.1; 1.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIB; 1.
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357 AVPA 360
                                                          604 ALLA 607
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01-MAY-1992
15-JUL-1999
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60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 IKAVALGAAGFLGVVSIDAPDMVMFLV-CAVVTFFIAFG-AAIAYGLYLVRRNGSIDPDA 177
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01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC LIABC COMPONENT (ELIABC-BGL)
PETA-GLUCOSIDES-PERMEASE LIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
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Bramley H.F., Kornberg H.L.;
"Nucleotide sequence of bglC, the gene specifying enzymeIIbgl of
"Nucleotide sequence of splC, the gene specifying enzymeIIbgl of
PEP:sugar phosphotransferase system in Escherichia coli K12, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL 349
                                                                                                                                                                                                                                                                                                                                                                                                               Length 631;
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J. Gen. Microbiol. 133:563-573(1987).
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PTSB_STAXY
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                                                                                                                                              SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE. SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
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Probom; PD002243; PTS_EIIB; 1.
PROSITE; PS00311; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIE_CYS; 1.
PROSITE; PS01035; PTS_EIIE_CYS; 1.
Phosphorransferase system: Sugar transport; Transferase;
Phosphorylation; Transmembrane; Inner membrane; Complete proteome.

EIIB DOMAIN.
                              Schnetz K., Toloczyki C., Rak B.;
Beta-glucoside (bgl) operon of Escherichia coli K-12: nucleotide
"Sequence, genetic organization, and possible evolutionary
relationship to regulatory components of two Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                              ON BGLG.
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SIMILARITY).
SIMILARITY).
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FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON BG
CATALIXIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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PHOSPHORY LATION
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                                                                                                                   Bacteriol. 169:2579-2590(1987)
               MEDLINE-8722180; Pubmed=3034860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOGENCY EQUILS; BOJF.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00358; PTS_EIIA_1; 1.
Pfam; PF00357; PTS_EIIB; 1.
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PIR, C25977; C25977.
PIR; A47616; A47616.
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24
306
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1120
1161
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223
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345
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24
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EMBL; 1
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                                                                                                     genes.
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Stabhylococcus xylosus.";
Mol. Gen. Genet. 241:33-41(1993).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
-SUGAR PHOSPHOTRANSFERAGE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS SITE
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA PRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD-ATAAPVPAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 35, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC. 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                          EKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 PSIFTFMQTIPSTGIDFTVWASV ----IGGVIAIGCAFV --- GTVMLHFITAKROPAOG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagner E., Goetz F., Brueckner R.; "Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system from
                                                                                                                                                                                                                                                                                                                                         GLLFGLVYSPIVITGLHQSFPPIELELFN-QGGSFIFATASMANIAQGAACLAVFFLAKS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR -
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APQEKTPEVITPPEQGGICSPMTGEIVPLIHVADTTFASGLLGKGIAILPSVGEVRSPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 TKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC
                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                       Length 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                 ; Score 450; DB 1; Length 62; Pred. No. 1.1e-24; 64; Mismatches 154; Indels
                                                                                                                                                           9E12A2207125C4E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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                             POTENTIAL
                                                   POTENTIAL
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MEDLINE-94049686; PubMed-8232209;
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                                                                                                                                                                                                                                    24.7%;
33.3%;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3%
Matches 116; Conservative
                                                                                                                                                             66482
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375
401
424
452
510
546
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                                                                                                                                                           625 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
355
381
404
432
490
526
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P51184;
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85;
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P22825;
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

1. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMANNS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-BERNATERSE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC 2.7.1.69) (EII-SCR).
SCRA OR PTSB OR PM1846.
                                                                                                                                                                                                                                                                                                                                                                                                                            ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ALFNIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                   DB 1; Length 480;
                                                                                                                                                                                                                                          ELIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
AB4ELD9785D84E47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE SUGAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                        47; Indels
                                                                                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                                  24.5%; Score 446.5; DB 1
52.5%; Pred. No. 1.4e-24;
ive 30; Mismatches 47
                                                                                                                                                                                                        Phosphotransferase system; Sugar transport; Tra
Transmembrane; Inner membrane; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN
                                                                                                                                                                                                                                EIIB DOMAIN
                                                                                                                                                                              ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21145866; PubMed-11248100;
                                                                                                                               InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                             51326 MW;
                                                                                                                    EMBL; X69800; CAA49461.1;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52...
893; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                          480
26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella multocida
                                                                                                                                                                                                                                                                             480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=747;
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SEQUENCE
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MOD_RES
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                                                                                                                                                                                                                                 DOMAIN
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01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC INCECCOMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE INC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(BC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane, Phosphorylation; Complete proteome.

PELIB DOMAIN.

POTENTIAL.

POTENTIAL.

POTENTIAL.
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NCBI_raxID=663;
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D26FA1A059603C01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.0%; Score 418; DB 1; 50.9%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA
                                                                         SIMILARITY: CONTAINS A PTS EIIB DOMAIN. SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                      EMBL; AE006222; AAK03930.1; -.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphotransferase system; Transferase;
Transmembrane; Inner membrane; Phosphory
PROTEIN HISTIDINE + SUGAR PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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474 AA;
                                                    (BY SIMILARITY)
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Best Local Similarity
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71626
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364
397
462
462
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                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-ATCC 13869;
                                                                                                                                               Corynebacterium.
NCBI_TaxID=1718;
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                                                                                                        Plasmid pBSBG2
                                                                                                                                                                                                                                                                                                                                                                   THE SUGAR.
                                                                                                                                                                                                                      Yoon K.-H.;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                      SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE ITCD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHORH); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                     SEQUENCE OF 1-12 FROM N.A.

MEDLINE=91285433; PubMed=2060795;
Blatch G.L., Woods D.R.;

Nucleotide sequence and analysis of the Vibrio alginolyticus scr
repressor-encoding gene (scrR).";

Gene 101:45-50(1991).

-I. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
latch G.L., Scholle R.R., Woods D.R.; Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCA-VVTFFIAFGAAIAYGL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00367; PTS_EIB; 1.
Pfam; PF00378; PTS_EIIC; 1.
Prodom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIB_CYS; 1.
Phosphotransferase system; Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBF906B5170E3EB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 1;
3.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIIB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 412; 49.7%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M76768; AAA27555.1; -.
EMBL; M35009; AAA27557.2; -.
PIR; JQ0781; JQ0781.
HSSP: P05051; JIBA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTGA_CORGL STANDARD;
Q45298;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49890 MW;
                               uptake-encoding region.";
Gene 95:17-23(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                              THE SUGAR.
   Blatch G.L.,
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MOD_RES
SEQUENCE
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PTGA_CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
20-NG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, GLUCOSE-SPECIFIC IABAC COMPONENT (EIIABC-GLC) (GLUCOSE-PERWEASE IABAC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-GLC/FIII-GLC).
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PHOSPHORYLATION (BY SIMILARITY).
67A75AAF76E42FA2 CRC64;
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PRODOM; PD00243; PTS_ELIA, -
ROSTITE; PS01037; PTS_ELIA, 1; 1.
R PROSTITE; PS01035; PTS_ELIB_CYS: 1.
W Phosphotransferase system; Sugar transport; Transferase;
KW Phosphorylation; Transmembrane; Plasmid.
FT DOMAIN 1 43 EIIB DOMAIN.
FT DOMAIN 7 PILE DOMAIN.
FT DOMAIN 7 PILE DOMAIN.
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacteriaceae,
                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum (Brevibacterium flavum).
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00358; PTS_EIIC.
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ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD002243; PTS_EIIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L18875; AAA22992.1; -.
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7 VGGLLFGLVYSPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFFL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
18.1%; Score 330; DB 1; Length 470;
Best Local Similarity 41.6%; Pred. No. 2.4e-16;
Matches 67; Conservative 34; Mismatches 58; Indels
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"Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region
                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                         482 QINNTPAAPAAPAAPAAGAAAAGGAAGAT-AVATKPRLAAGQLVEITSPLEGHAVPLSEV 540
                                                                                                                                                                                                                                                                                                                       307 IVIPLLYPFLVPLGLHWPLNAIMIQNLNTLGYDFIQGPMGAWNFACFGLVTGVFLIALKE 366
                                                                                                           69 KLKGLAGAS--GVSAVL--GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA 124
                                                                                                                                                                                                                                                                                                          279 FDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY 338
                                                                                                                                                                                   F---VFTSLLTIPAMDPWLGYTVGIAAAF--FTSMLLVLFFDYRSDAERDEAKAQMAAAE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoock F., Dahl M.K.;
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals genes encoding a putative specific enzyme IITre and a potential regulator of the trehalose operon.";
Gene 175:59-63(1996).
                                     Gaps
                                                            10 LLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
Microbiology 142:3057-3065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                          PTTB_BACSU STANDARD; PRT; 470 AA.
P39794; 034771;
01-FEB-1995 (Rel. 31, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
PROBABLE PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE)
(TREHALOSE-PERMESE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, COMPONENT) (EC 2.7.1.69) (EII-TRE).
                                                                                                                                                            125 LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----
                                                                                                                                                                                                                                                           SDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIG
                                                                                                                                                                                                           ----PDATAAPV-----PAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSV
                                     41;
            Length 674;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.NCBI_TaxID=1423;
            DB 1;
                                   61; Mismatches 156;
                        6e-20;
           21.2%; Score 386.5; 31.0%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
MEDLINE-97074649; PubMed-8917076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97417488; PubMed=9272861;
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                                     Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                         339 GLGEIEAGANLLNV 352
                                                                                                                                                                                                                                                                                                                                                                                  657 EAAQADATTTVIKV 670
                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREP OR TREB.
Bacillus subtilis.
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            Query Match
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                                                                                                                                                                                                                Helfert C., Gotsche S., Dahlm.K.;

"Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by a phospho-alpha (1-1)-glucosidase encoded by the treA gene.";

Mol. Microbiol. 16:111-120(1995).

I. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS COMPAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
or the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and general stress response protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR -
PROPEIN HISTIDINE + SUGAR PHOSPHATE.
-!- SUBCELLULAR LOCATION: INTEGRAL PREBRANE PROTEIN. INNER MEMBRANE.
-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Complete proteome.
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EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Sugar transport; Transferase;
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M -> L (IN REF. 1 AND 4).

A -> G (IN REF. 1 AND 4).
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                                                                                                                                                                                                MEDLINE=95379486; PubMed-7651129;
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EMBL, D86417; BAA22289.1; --
EMBL, X80203, CAA56494.1; --
EMBL, 299108, CAB12609.1; --
HSSP, P05053, 118A.
Subtilist, BG11009; treP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
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                                                                                                                                                SEQUENCE OF 324-470 FROM N.A.
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                                                                                           Gene 194:191-199(1997).
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470 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. Gen. Genet. 230:270-276(1991).

-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO
                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC ITABC COMPONENT (EIIABC-NAG)
(N-ACETYLGLUCOSAMINE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-NAG).
VKDEKQKGLSLTSGISAYLGITEPAIFGVNLRYRFPFIIAMVSSGLAGMYISSQGVLASS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                       65 AKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparison of the sequences of the nagE operons from Klebsiella pneumoniae and Escherichia coli K12: enhanced variability of the enzyme IIN-acetylglucosamine in regions connecting functional
                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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                                                                                               LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLY 165
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SIMILARITY: CONTAINS A PTS ELIB DOMAIN.
SIMILARITY: CONTAINS A PTS ELIC DOMAIN.
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                                                                                                                                                                                               PRT;
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MEDLINE-92079906; Pubmed-1745234;
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001332; PTS_EIIC.
Pfam; PF00158; PTS_EIIA.1; 1.
Pfam; PF00267; PTS_EIIB; 1.
Pfam; PF002378; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; PD001476; PTS_EIIB; 1.
Probom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS;
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                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08837
                                                                                                                                                                                                                                                                                                                                                      Klebsiella.
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P45604;
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20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYGTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(RC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......GL----- 164
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                                                                                                                                                                                                                                                                                                            ------GVNLRLRWPFFIGIGTAAIGGAL--IALFNIKAVALGAAGFLGVVSIDAP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVWMLLVMGVVFFFVYFLLFSAVIRMFNLKTPGREDKAADVVTEEANSNTEEGLTQLATS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 YIAAVGGTDNLKAIDACITRLRLTVGDSAKVNDAACKRLGASGVVKLNKQTIQVIVGAKA 455
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                              -- ELELFNOG----GSF 42
                                                                                                                                                                                                                                                                                                                                              43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-----
                                                                                                                                                                                                                                                                                                                                                            290 LLYLLHAVLTGISLFIATALGIHAGFSFSAGAIDYVLMYSLPAA------SK
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                                                                                                                                                                                                                                                                       Indels 166;
                                     SIMILARITY).
SIMILARITY).
                          SIMILARITY).
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3D8D8ADFF4BD48ED CRC64;
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                                    PHOSPHORYLATION PHOSPHORYLATION POTENTIAL.
             EIIA DOMAIN.
PHOSPHORYLATION
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 337 TYGLGEIEAG 346
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PTSB_BACSU
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STRAIN=168
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A Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
A Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
A Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
A Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
A Rapoport G., Danchin A.;
A Rapoport G., Danchin B.;
A Rapoport G., Danchin G., The PHOSPHOENOLPPRUVATE-DEPENDENT G. TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEBRAE SYSTEM, THE IICD DOMAINS CONTAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DOMOR IS PHOSPHORYLERS): IIA TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
SIMILARITY: 57% IDENTITY WITH THE NEGATIVE REGULATORY PROTEIN OF
                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON SACT (BY
                                                             SEQUENCE FROM N.A.
MEDLINE=88097369; PubMed=3122206;
Fouet A., Arnaud M., Klier A., Rapoport G.;
"Bacillus subtilis sucrose-specific enzyme II of the phosphotransferaes system: expression in Escherichia coll and homology to enzymes II from enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 84:8773-8777(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphotransferase system; Sugar transport; Transferase; Transmembrane; Phosphorylation; Complete proteome.

BIND DOMAIN
             Bacteria; Firmicutes; Bacillus/Clostridium group;
                     Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIIC DOMAIN
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PIR: S39704; S39704.

HSSP: P05053; 11BA.

InterPro; IPR001996; PTS_EIIB.

InterPro; IPR001352; PTS_EIIC.

Pfam: PF0057; PTS_EIIE.

ProDom; PD001476; PTS_EIIB; 1.

PROSTIE: PS01035; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03006; AAA22727.1; -.
EMBL; X73124; CAA51605.1; -.
EMBL; Z99123; CAB15831.1; -.
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26
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133
168
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60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                  29
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P20166; P08875;
01-NOV-1988 (Rel. 09, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-GLC/EIII-GLC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonzy-Treboul G., Zagorec M., Rain-Guion M.C., Steinmetz M.; "Phosphoenolpyruvate:sugar phosphotransferase system of Bacillus subtilis: nucleotide sequence of ptsX, ptsH and the 5'-end of ptsI
                                                                                                                                                                                                                                                                                                                                                               1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACL
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                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reizer J.,
                                                                                                                                                                                                                          Length 460;
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MEDLINE-92001991; PubMed~1911744;
Liao D.-I., Kapadia G., Reddy P., Saier M.H. Jr., Reizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 IKAVALGAAGFLGVVSIDAP----DMVMFL----VCAVVTFFIAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | | | : :::| || : :::| || | || || 405 VAANAYGLTG-IPMIAIAAPFGFSNLIHYLIGMAIAAVSAFIAAF 448
                                                                                                                                       6A303DC042BFE379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                       ; DB 1;
1.4e-14;
                                                                                                                                                                                                                    16.7%; Score 305; DB
44.8%; Pred. No. 1.4e
Live 25; Mismatches
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Mol. Microbiol. 3:103-112(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89237891; PubMed=2497294;
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STRUCTURE BY NMR OF EIIA DOMAIN.
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Biochemistry 30:9583-9594(1991)
                                                                                                                                       49002 MW;
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348
378
406
427
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                                                386
407
429
460 AA;
                                                                                                                                                                                                                                                 Local Similarity
nes 74; Conserv
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                                                                                                                                                                                                                 STRUCTURE BY NAR OF EIAA DOMAIN.

STRUCTURE BY NAR OF EIAA DOMAIN.

MEDLINE-98254029; PUBMEd=9593107.

Chen Y., Case D.A., Reizer J., Saier M.H. Jr., Wright P.E.;

"High-resolution solution structure of Bacillus subtilis IIAglc.";

Proteins 31:258-270 (1998).

-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO
      Fairbrother W.J., Cavanagh J., Dyson H.J., Plamer A.G. III,
Sutrina S.L., Reizer J., Saier M.H. Jr., Wright P.E.;
"Polypeptide backbone resonance assignments and secondary structure
of Bacillus subtilis enzyme IIIglc determined by two-dimensional heteronuclear NMR spectroscopy.";
                                                                                                                                                     CATALTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
SIMILARITY: CONTAINS A PTS EIB DOMAIN.
SIMILARITY: CONTAINS A PTS EILE DOMAIN.
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MEDLINE~91299743; PubMed=1906345;
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-----I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGTAAI --GGALIAL --FNIK -----AVALGAAGFLGVVSIDAPDMVMFLVCAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Mismatches 134; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 2A14D3C32EE0A9C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.4%; Score 299; DB 1; 24.3%; Pred. No. 5.9e-14;
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Matches 119; Conservative
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InterPro; IPR003352; PTS_EIÍC.
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RA MEDLINE-91100329; Pubbed=1846143;

Rat Hardesty C., Ferran C., Direnzo J.M.;

Hardesty C., Ferran C., Direnzo J.M.;

Hardesty C., Ferran C., Direnzo J.M.;

Hardesty C., Ferran C., Direnzo J.M.;

Tobamid-mediated sucrose metabolism in Escherichia coll:

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Tobamid-mediated sucrose Transport system.

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                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1996 (Rel. 34, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of the gene scrA encoding the sucrose transport protein EnzymaII(Scr) of the phosphotransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Bgl) proteins."; Mol. Microbiol. 2:9.17(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jahreis K., Lengeler J.W.; "Molecular analysis of two ScrR repressors and of a ScrR-FruR hybrid repressor for sucrose and D-fructose specific regulons from enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                            456 AA.
                                                                         PRT;
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EMBL; Y00041; CAA68605.1; ALT_SEQ.
EMBL; M38416; AAA98418.1; -.
PIR; S01036; WQEBST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-88216186; Pubmed-3285123;
Ebner R., Lengeler J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94018607; PubMed-8412665;
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InterPro; IPR001996; PTS_EIIB.
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                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
Plasmid pUR400.
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                                                                         PTSB_SALTY
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                                                                                                      P08470;
                       RESULT 14
PTSB_SALTY
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MEDLINE=88212176; PubMed=3284790;
Rogers M.J., Ohgi T., Plumbridge J., Soell D.;
Rogers M.J., Ohgi T., Plumbridge J., Soell D.;
Rolectide sequences of the Escherichia coli nagE and nagB genes:
the structural genes for the N-acetylglucosamine transport protein of
the bacterial phosphoenolpyruvate: sugar phosphotransferase system
and for glucosamine-6-phosphate deaminase.";
                                                                                                                                                                                                                                                                                                                                                            349 WFKTKDAKIKAITLPSAFSAMLGITEAAIFGINLRFVKPFIAALIGGAAGGAWVVSVHVY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC COMPONENT (EIIABC-NAG)
N-ACETYLGLUCOSAMINE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II. ABC COMPONENT) (EC 2.7.1.69) (EII-NAG).
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                       5 GPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ---GGSFIFATASMANIAQGAACLAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1655;
STRAIN-KIZ. / MG1655;
Pubbed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
Probom; PF001476; PTS_EIIC; 1.
PROSTITE; PF00135; PTS_EIIB_CYS; 1.
PROSTITE; PF035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Transferase; Sugar transport; Plasmid; Transmembrane; Inner membrane; Phosphorylation.

DOMAIN 1. ? EIIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY). PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                          DB 1; Length 456;
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                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                 98A6F1620AE50885 CRC64;
                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 MTAVGLTAIPGMAIVQASSLLNYIIGMVIAFGVAFTVSL 447
                                                                                                                                                                                                                                                          16.3%; Score 296.5; DB 1
40.3%; Pred. No. 5.4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 27:6054-6061(1988).
                                                                                                                                                                                                 47864 MW;
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Matches 64; Conserv
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1E24C97CFCBBAA59 CRC64;

68346 MW;

648 AA;

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Search completed: March 21, 2002, 16:28:51 Job time: 331 sec
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                                                      A Shima T., Alba H., Baba T., Fullta K., Hayashi K., Honjo A.,

A Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

A Kimura S., Kitaqawa M., Makino K., Masuda S., Mikir T., Mizobuchi K.,

A Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

A Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

A Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

A Mori H., Motomura K., Nakamura Y., Nashimoto Y.,

A 718-bb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 12.7-28.0 min region on the linkage map.";

LDA Res. 3137-155(1996).

CONFORTINE THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT

SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS). A MAJOR CARBOHYDRATE ACTIVE

TRANSFORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE

AND THE TRANSMEMBRARE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY

PHOSPHORYLATION SITE THE DOMOR IS PHOSPHO-HER): ITA TRANSFERS IT SO

MIND SHORY CONTAINS THE SHORD TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR HSSP; PO8837, 2F3G.
DR HSSP; PO8837, 2F3G.
DR ECGEne; EG10635; nagE.
DR InterPro; IPR001127; PFS_EIIA.
DR InterPro; IPR001327; PFS_EIIA.
DR InterPro; IPR001396; PTS_EIIA.
DR Pfam; PP00378; PTS_EIIA.1; 1.
DR Pfam; PP00378; PTS_EIIB; 1.
DR ProDom; PD001476; PTS_EIIB; 1.
DR ProDom; PD001476; PTS_EIIB; 1.
DR ProDom; PS001378; PTS_EIIA; 1.
DR PROSITE; PS01037; PTS_EIIA; 1.
DR PROSITE; PS01037; PTS_EIIA.1; 1.
EIIE DOMAIN.
TRANSMEMBRANE; SUBMAIN.
TRANSMEMBRANE; EIIB DOMAIN.
THOMAIN 393 427 EIIB DOMAIN.
THOMAIN 393 HAZ7 EIIB DOMAIN.
THOMAIN SIMILARITY).
                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
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EMBL; AE000171; AAC73773.1; -.
EMBL; D90770; BAA35322.1; -.
PIR; B29895; WORC2N.
PIR; A28896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283
                                                   Gaps
                                                                                                  5 GPVGGLLFGLVYSPIVITGLHQSFPPI -------ELELFNQG----GSF 42
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                                                                                                                                                                                                  43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-----
                                              62; Mismatches 162; Indels 154;
                                                                                                                                                                                                                                                                                                    -------CVNLRLRWPFFIGIGTAAIGGAL---------
Score 295; DB 1; Length 648;
Pred. No. 1e-13;
  16.2%;
23.2%;
  Query Match 16.2
Best Local Similarity 23.2
Matches 114; Conservative
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GenCore version 4.5
Copyright (c.) 1993 - 2000 Compugen Ltd
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protein search, using sw model ı OM protein

Run on:

US-09-604-231-4 1821 1 YDFGGPVGGLLFGLVYSPIV......IEAGANLLNVAKKEAVPATP 362

score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phosphotransferase	phosphotransferase	PTS system, beta-q	system,	S	beta-qlucoside per	hypothetical prote	beta-glucoside-spe	phosphotransferase	hypothetical prote		PTS system, sucros	sucrose uptake pro	PTS system, trehal	phosphotransferase	hypothetical prote		phosphotransferase	PTS system, sucros	phosphotransferase	phosphotransferase	phosphotransferase	hypothetical prote	phosphotransferase	sac operon requlat	phosphotransferase	PTS system, glucos	levansucrase synth	· PTS system, glucos
SUMMARIES	ΩI	E E	S44257	Нβ		868599			B42603											H83881		_	3		S		WQEBST			
	Length DB				636 2														651 1											
do	Query Match L	39.0	38.8		30.2		28.3		27.0	24.7	24.6	24.5	22.8	22.6	19.2	18.1	17.2	17.2	17.2	17.0	16.7	16.4	16.2	16.1			15.2			14.9
	Score	711	706.5	562.5	550.5	515.5	515	503	492.5	450	448	446.5	416	412	350.5	330	314	313.5	313	310	305	299	295	294	293.5	290	277.5	276	273	271.5
	Result No.		7	m	4	S	9	7	<b>6</b> 0	თ	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	56	27		53

phosphotransferase	phosphotransferase	phosphotransferase	phosphotransferase	lactose transport	phosphotransferase	phosphotransferase	PTS system, glucos	PTS system, glucos	phosphotransferase	PTS system, trehal	PTS system enzyme	phosphotransferase	phosphotransferase	probable phosphotr	raffinose carrier
D69750	S46952	70169	H69940	A32241	C65236	WQECP3	D85884	G82257	WQEB3T	B82263	A86122	G64137	B84937	C83177	S44253
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	14.8 675 1				13.7 473 2										
14.9						13.5		13.5		13.4		13.1	12.7	12.4	

## ALIGNMENTS

C.Keywords: phosphoprotein; phosphotransterase F.511-664/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho

8 24; Gaps Length 664; Ouery Match 39.0%; Score 711; DB 1; Length 664; Best Local Similarity 42.1%; Pred. No. 5.4e-43; Matches 155; Conservative 73; Mismatches 116; Indels

1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL---FNQG---GSFIFATASMANIAQ 54 ŏ

55 GAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGAL 114 q οy

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115 IALFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID 174 Dp δy

175 PDATAAPVPAGTTKAEAEAPAEFSNDST-----IIQAPLTGEAIALSSVSDAMFASGK 227 Οy

q

228 LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGT 287 δy

QQ

288 HFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY-GLGEIEAG 346 597 GFEQKVQADQKIKKGDVLGTFDSDKIAEAGLDNTTMFIVTNTADYASVETLASSGTVAVG 656 δy

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347 ANLLINVAK 354 ò

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Length Indels

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PTS 593 per december 2001 per 2000 per 2001 per 2000 per 
C; Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 IKAVALGAAGFLGVVSI---DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : | | : | | : | | : | 457 DILSNESGSENEVKREDDKKEPSASEEIKSPLKGEVVPLTEVQDHVFSSGAMGKGVAVRP 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 296
                                                                                                                                                                                                                                                                                                                                                                          60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                                             177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 KEGRLVAPINGTVTSLFETKHAIGITS----DNGTEIFIHVGIDTVQLKGEHFTSFIEQG 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQGYIIGGLGIFGIPSFLHPADGMDAGFWGIVIAVVVAFV-LGFILTYLFGLKSGNASDE 472
                                                                                                                                                                                                                                   1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                                                                                               30.9%; Score 562.5; DB 2; 34.6%; Pred. No. 1.8e-32; 1ve 78; Mismatches 143;
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                                                                                               Query Match 30.9%;
Best Local Similarity 34.6%;
Matches 124; Conservative
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C:Species: Bacillus halodurans
C:Species: Bacillus halodurans
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: H8368
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Accession: H8368
A:Accession: H8368
A:Status: preliminary
A:Residues: 1-630 <STO>
A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04015.1; GSPDB:GNOC C:Genetics:
BH0296
A:Genetics:
A:Genetics:

    Pediococcus pentos

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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
C;Keywords: phosphotransferase
F;488-640/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
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                               pnosphotransferase system enzyme II (EC 2.7.1.69), sucrose specific - Pediococcus p C; Species: Pediococcus pentosaceus C; Deter: 19-mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999 C; Accession: 544.257
R; Leenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G. submitted to the EMBL Data Library, April 1994
A; Description: The sucrose and raffinose operons of Pediococcus pentosaceus PPEI.0. A; Reference number: $44.252
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-651 <LEE>
A;Cross-references: EMBL:Z32771; NID:g493728; PIDN:CAA83668.1; PID:g475968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.8%; Score 706.5; DB 2; Length 42.0%; Pred. No. 1.1e-42; Live 64; Mismatches 126; Indels
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Best Local Similarity 42.0%
Matches 154; Conservative
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: preliminary; nucleic acid sequence not shown; A; Status: preliminary; No. 7, 76-182 cast.
A; Residues: 1-74, 52, 76-182 cast.
A; Cross -references: EMBL: X85408; NID:g1037169; PIDN:CAA59697.1; PID:g1037172
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
B; Nunst, F; Ogaswara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, CV; Caldeul, B; Capusno, V; Carter, N.M;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, Nature 390, 240-256, 1997
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal sch, J; Harwood, C.R; Henaut, A; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardino A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Leevine, A; Liu, H; Mssuda, S; Mau S, Authors: Lauber, J; Lazarevic, V; Lee, S.M; Sadaje, Y; Sato, T; Scanl A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Seklquchi, J; Scato, T; Scanl A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Seklquchi, J; Scato, Y; V; U; Haiter, The complete genome sequence of the Gram-positive bacterium Bacillus subtill A; Reference number: A69580; MuID:98044033
A; Reference number: A69580; MuID:98044033
A; Residues: I-287, F', 289-433, 'G', 435, 'S', 437-448, 'HR', 451-548, 'M', 550-551, 'S', 553-60
A; Cross-references: GB:29924; GB:A009126; NID:92636442; PIDN:CABIS963.1; PID:926364
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
F;458-609/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
                                                                                                                                                                                                                           Escherichia coli
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                                                                                                               PIDN:CAA84286.1; PID:9505576
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A;Title: Suppression of the Bgl+ phenotype of a Delta-hns strain of A;Reference number: 865579; MuID:96204517
A;Reference number: 865579;
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Pred. No. 4e-29;
3; Mismatches 142; Indels
   preliminary; translated from GB/EMBL/DDBJ
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33.2%; Pred
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Best Local Similarity
Matches 121; Conserv
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C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 20-Jun-2000
C; Accession: 140406; S65581; A69594; S47174
R; Le Coq, D.; Lindner, C.; Kruger, S.; Steinmetz, M.; Stulke, J.
A; Title: New Detarglucoside (bg1) genes in Bacillus subtilis: the bg1P gene product has A; Reference number: 140404; MUID:95189730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAV 61
                                          |::|:| || || |: | | || |: |
521 EPSEGKLFSPVSGMVTALYPTHHALGITT----DRCAELLIHIGLDTVQLDGKFFTAHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
                                                                                                                                                      QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.3%; Score 515.5; DB 2; 36.3%; Pred. No. 3.9e-29; ive 63; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 36.3
Matches 128; Conservative
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A; Gene: arbF C; Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera F;479-631/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the PEP:su
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Reference number: A91833; MUID:87222180
A.Accession: C25977
A.Molecule type: DNA
A.Molecule type: DNA
A.Kesidues: 1-625 < SCH>
A.Cross-references: GB:M16487; GB:M60288; NID:g145414; PIDN:AAA23510.1; PID:g145418
R.Bramley, H.F.; Kornberg, H.L.
J. Gen. Microbiol. 133, 563-573, 1987
A.Tille: Nucleotide sequence of bglc, the gene specifying enzymeII(bgl) of the PED:s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A47616
A;Status: preliminary
P;Moleule type: DNA
A;Residues: 1-625 <BRA>
A;Ross-references: GB:MI5746; NID:g145412; PIDN:AAA83837.1; PID:g145413
A;Cross-references: GB:MI5746; NID:g145412; PIDN:AAA83837.1; PID:g145413
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, I.A.; Rose, D.J.; Mau, B.; Sho, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: C65175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 YGLNSLLAGAVMGALWQVCVIFGLHWGFVPLMLNNFSVIGHDTLLPLLVPAVLGQAGATL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 IKAVALGAAGFLGVVSIDAPDMVMFLV-CAVVTFFIAFG-AAIAYGLYLVRRNGSIDPDA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 GVLLRTQDLKRKGIAGSAFSAAIFGITEPAVYGVTLPLRRPFIFGCIGGALGAAVMGYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 AAADSPA--VLAETQANAGAVRDETLF-SPLAGEVLLLEQVADRTFASGVMGKGIAIRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                             62; Mismatches 154;
                                                                                                                                                                                                                                                                                 27.0%; Score 492.5; DB 34.9%; Pred. No. 1.7e-27
                                                                                                                                                                                                                                                                                      Query Match 27.0%
Best Local Similarity 34.9%
Matches 123; Conservative
C; Genetics:
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R;el Hassouni, M.; Henrissat, B.; Chippaux, M.; Barras, F.
J. Bacteriol. 174, 765-777, 1992
A;Title: Nucleotide sequences of the arb genes, which control beta-glucoside utilization olase family including enzymes from eubacteria, archeabacteria, and humans.
A;Reference number: A42603; MUID:92121114
A;Recession: B42603
A;Ratus: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-631 < ELL>
A;Cross-references: GB:M81772; NID:g148385; PIDN:AAA24814.1; PID:g148387
A;Note: sequence extracted from NCBI backbone (NCBIN:77535, NCBIP:77537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
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C;Species: Erwinia chrysanthem1
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conta
                                                                                                                                                                                                                          C; Species: Bacillus subtilis
C; Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C; Accession: T47097
R; Yoshida, K.; Sano, H.; Seki, S.; Oda, M.; Fujimura, M.; Fujita, Y.
Microbiology 141, 337-343, 1995
A; Title: Cloring and sequencing of a 29 kb region of the Bacillus subtilis genome A; Reference number: 224350; MUID: 95219088
A; Reference number: 224350; MUID: 95219088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 GQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 VKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKK--TGPVNTYGLGEIEAGANLLNVAKKE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG-SFIFATASMANIAQGAACL 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches 139; Indels
                                                                                                                                                                                 hypothetical protein N17C [imported] - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%; Score 503; DB 2; 33.5%; Pred. No. 2.9e-28;
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C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: F82432
R; Heidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-479 <hEI>
A;Cross-references: GB:AE004395; GB:AE003853; NID:g9658068; PIDN:AAF96554.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the scrA gene encoding the sucrose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F82432
PTS system, sucrose-specific IIBC component VCA0653 [imported] - Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Staphylococcus xylous
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S39978; E: Brueckner, R.
Mol. Gen. Genet. 241, 33-41, 1993
A;Title: Cloning and characterization of the scrA gene encoding the sucrose-A;Reference number: S39976; MUID:94049686
A;Accession: S39978
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X69800; NID:9407905; PIDN:CAA49461.1; PID:9407908 C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ALFNIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ
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C;Superfamily: phosphotransferase system sucrose-specific enzyme II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%; Score 446.5; DB 2; 52.5%; Pred. No. 2.2e-24; 1ve 30; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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52.4%; Pred. No. 3.2e-22;
iive 26; Mismatches 48;
                                                                                                                                                                                                                 296 GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
                                                                                                                                                                                                                                                                                                                                                                                                                        scrA protein - Staphylococcus xylosus
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Best Local Similarity 52.47
Matches 86; Conservative
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Best Local Similarity
Matches 93; Conserv
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S39978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein ptbA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001 C;Accession: D86807 C;Accession: D86807 C;Accession: D86807 C;Arcer, P.; Mandger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrligenome Ress. in press, 2001 A;File: The complete genome sequence of the lactic acid bacterium. A;Accession: D86807 A;Status: preliminary A;Accession: D86807 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-636 csTo> A;Cross-references: GB:AE005176; NID:g12724452; PIDN:AAK05558.1; GSPDB:GN00146 A;Experimental source: strain IL1403 C;Genetics: A;Genetics: A;Geneti
C;Keywords: phosphoprotein; phosphotransferase; transmembrane protein F:473-625/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD-ATAAPVPAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSIFTFMQTIPSTGIDFTVMASV----IGGVIAIGCAFV---GTVMLHFITAKRQPAQG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKAEAREAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 APQEKTPEVITPPEQGGICSPWTGEIVPLIHVADTTFASGLLGKGIAILPSVGEVRSPVA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQCDEVKAGELLC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYTMGA---LGIFSFTSNITLTGEVSGALKIMIVSAVAVIAGFVVTYLV----GFEDDVI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAPVPAGTTKAEAEAPAEFSNDST---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIV 235
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                             9 GLLFGLVYSPIVITGLHQSFPPIELELFN-QGGSFIFATASMANIAQGAACLAVFFLAKS 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AQKKVVAGSAALTSLFGITEPAVYGVNLPRKYPFVIACISGALGATIIGYAQTKVYSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 636;
                                                                                                                                              Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                          Indels
                                                                                                                                      24.7%; Score 450; DB 2; Le
33.3%; Pred. No. 1.7e-24;
ive 64; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 448; DB 2;
llarity 33.0%; Pred. No. 2.4e-24;
Conservative 59; Mismatches 136;
                                                                                                                                   Ouery Match
Best Local Similarity 33.38,
Matches 116; Conservative
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Best Local Simil
Matches 110; C
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Cypecies: Bacillus subtilis
C;Species: GS-02-1997 **Sequence_revision OS-0c-1997 **text_change 20-Jun-2000
C;Accession: C69725; S67929; JC5037; I40497; S67864
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
A;Authors: Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlya
T.; Winters, P.; Winters, P.; Winpat, A.; Yamanec, K.; Yamane, K.; Yasumoto, W.; Yasumoto, M.; Yamane, K.; Yasumoto, W.; Wanner, M.; Tasako, K.; Yasumoto, M.; Amanes, M.; Atte, Danchin, A.; Tosato, W.; Alters, P.; Winters, P.; Winpat, A.; Yamanec, M.; Yasumoto, M.; Yasumoto, M.; Yasumoto, M.; Yasumoto, M.; Aranako, M.; Atters, P.; Winters, P.; Winters, M.; Selosime Sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
A; Reference number: A69580; MUID:98044033
A; Maters, mucleic and sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: DNA
A; Residues: 1-470 < KUNN
A; Cross references: GB: 299108; GB: AL009126; NID: 92633055; PIDN: CAB12609.1; PID: 926331
A; Experimental source: strain 168
B; Helfert, C.; Gotsche, S.; Dahl, M.K.
Mol. Microbiol. 16, 111-120, 1995
A; Title: Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by a phosp
A; Reference number: 140497; MUID: 95379486
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A;Cross-references: EMBL:254245; NID:g1000450; PIDN:CA91014.1; PID:g1000451
C;Comment: This enzyme functions as the specific trehalose transporter. It belongs
C;Genetics:
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                                                                                                                                                                                                                 KSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 125
                                                                                                                                                          7 VGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLA 65
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     Pred. No. 1.4e-17;
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A;Residues: 324-362,'L',364-464,'G',466-470 <HEL>
A;Cross-references: EMBL:X80203; NID:9580941
R;Schoeck, F.; Dahl, M.K.
Gene 175, 59-63, 1996
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GAAGFLGVVSIDAPDMVMFLVCAVVTFFI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
     46.38;
                                                 Conservative
Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sucrose uptake protein - Vibrio alginolyticus
N.Alternate names: enzyme II-sucrose protein
C.Spetos: Vibrio alginolyticus
C.Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 18-Jun-1999
C.Accession: J00781
R.Blatch, G.L.; Scholle, R.R.; Woods, D.R.
Gene 95, 17-23, 1990
A.Title: Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose uptake-enc
A.Reference number: J00781
M.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Status: Drallminary
A.Residues: 1-479 cala>
A.Residues: 1-479 cala>
A.Cross-references: GB:M76768; GB:M30194; NID:g155261; PIDN:AAA27555.1; PID:g155262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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A;Gene: BH2216
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
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1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA
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C;Superfamily: phosphotransferase system sucrose-specific enzyme II,
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1 Similarity 49.7%; Pred. No. 6.2e-22;
84; Conservative 32; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 160
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Best Local S
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enzyme II, factor II

Length 470;

DB 2;

Score 350.5;

19.28;

Query Match

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1;
Ouery Match 18.1%; Score 330; DB 2; Length 470;
Best Local Similarity 41.6%; Pred. No. 4e-16;
Matches 67; Conservative 34; Mismatches 58; Indels 2; Gaps
                                                                                                7 VGGLLFGLVYSPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFFL 64
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Search completed: March 21, 2002, 16:23:47 Job time: 153 sec

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Sequence 13467, A Sequence 13467, A Sequence 13467, A Sequence 13658, Ap Sequence 12270, A Sequence 12270, A Sequence 10089, A Sequence 10089, A Sequence 10500, A Sequence 10500, A Sequence 5822, Ap Sequence 5822, Ap Sequence 12942, A Sequence 12949, A Sequence 12
                                                                                                                                         (without alignments)
821.709 Million cell updates/sec
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1821
1 YDFGGPVGGLLFGLVYSPIV.....IEAGANLLNVAKKEAVPATP
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                                                                                                                   March 21, 2002, 16:27:36; Search time 29.76 Seconds
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USOG_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USOR_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USOR_NEW_COMB.pep:*

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-815-242-13467
US-10-072-813-13467
PCT-USO2-03987-5658
US-09-815-245-5658
US-09-815-245-5658
PCT-USO2-03987-12270
US-09-815-242-12270
US-10-072-851-12270
PCT-USO2-03987-10089
US-09-815-242-10089
US-09-897-516-6783
PCT-USO2-03987-10500
US-09-815-242-10500
US-09-815-242-10500
US-10-072-851-10500
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US-10-072-851-5822
PCT-US02-03987-12942
US-09-815-242-12942
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US-09-815-242-12479
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                                                                                                                                                                                                                                                                                                                                              322656 seqs, 67552660 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             protein search, using sw model
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Maximum DB s
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Sequence 12479, A	Sequence 11950, A	Seguence 11950, A	Sequence 11950, A	Sequence 13018, A	Sequence 13152, A	Sequence 13018, A	Sequence 13152, A	Sequence 13018, A	Sequence 13152, A	Sequence 5842, Ap	Sequence 5842, Ap		Sequence 10809, A	Seguence 10809, A	Seguence 10809, A	Sequence 5718, Ap	Sequence 5718, Ap	Sequence 5718, Ap	Sequence 12272, A
US-10-072-851-12479	PCT-US02-03987-11950	US-09-815-242-11950	US-10-072-851-11950	PCT-US02-03987-13018	PCT-US02-03987-13152	US-09-815-242-13018	US-09-815-242-13152	US-10-072-851-13018	US-10-072-851-13152	PCT-US02-03987-5842	US-09-815-242-5842	US-10-072-851-5842	PCT-US02-03987-10809	US-09-815-242-10809	US-10-072-851-10809	PCT-US02-03987-5718	US-09-815-242-5718	US-10-072-851-5718	PCT-US02-03987-12272
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12.6	12.4	12.4	12.4	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.1	12.1	11.1	11.1	11.1	10.5
229	226.5	226.5	226.5	221.5	221.5	221.5	221.5	221.5	221.5	220.5	220.5	220.5	220.5	220.5	220.5	201.5	201.5	201.5	190.5
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45

## ALIGNMENTS

RESULT

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ECT-USO2-03987-13467 : Sequence 13467. Ap	T-USO2-03987-13467 Sequence 13467, Application PC/TUS0203987
GENERAL INFORMATION:	AATON:
; TITLE OF INVE	TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inf
; TITLE OF INVENTION:	
; FILE REFERENC	FILE REFERENCE: ELITRA.OZBVPC Chrreni additoation nimmer. Dot/had2/02/03987
CURRENT FILING DATE:	WG DATE: 2002-02-02
; PRIOR APPLICA	APPLICATION NUMBER: 60/267,636
; PRIOR FILING	PRIOR FILING DATE: 2001-02-09
; SOFTWARE: Fas	NOTIFICATION OF THE PROPERTY O
; SEQ ID NO 13467	
; LENGTH: 62/	
ORGANISM: St	ORGANISM: Streptococcus pneumoniae
PCT-US02-03987-1	13467
Query Match	29.8%; Score 542; DB 1; Length 627;
Best Local Sim Matches 128;	Best Local Similarity 36.0%; Pred. No. 1.36-32; Matches 128; Conservative 74; Mismatches 130; Indels 24; Gaps 9;
Qy 3 FGGPVG	SGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAV 61
Db 288 FGLG	288 FGLGGFLIGGVHQLIVVSGVHHIFNLLEVQLLAADHANPFNAIITAAMTAQGAATVAV 345
Qy 62 FFLAKS	SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
Db 346 GVKTKN	NPKLKTLAFPAALSAFLGITEPAIFGVNLRFRKPFFLSLIAGAIGGGLASILGLA 405
Qy 122 AVALGA	122 AVALGAAGFLG-VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA 180
Db 406 GTGNGI	406 GTGNGITIIPGTMLYVGNGQLPQYLLMVAVSFALGFALTYMFGYEDEVDATAA 458
Qy 181 PVPAGT	TTKAEAE-APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKG 239
Db 459 AKQAEV	459 AKQAEVAEEKEEVAPAALQNETLVTPIVGDVVALADVNDPVFSSGAMGQGIAVKPSQG 516
Qy 240 QLVSPV	/SGKIVVAEPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEV 299
Db 517 VVYALA	:::   :   :   :: :::::::::::::::::::::
Qy 300 KAGELL	CEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNV 352
Db 573 KAGDVL	

us-09-604-231-4.rapn

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29.8%; Score 542; DB 7; Length 62 ilarity 36.0%; Pred. No. 1.3e-32; Conservative 74; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15811
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13467
LENCTH: 627
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Application US/10072851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptococcus pneumoniae US-10-072-851-13467
                                                                                                             Foulkes, J. Gordon
Zamudio, Carlos
                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                        Haselbeck, Robert
                                                        APPLICANT: Carr, Grant J. APPLICANT: Xu, H. Howard
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Best Local Similarity
Matches 128; Conserva'
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APPLICANT:
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-26
PRIOR PELING DATE: 2000-12-26
PRIOR PELING DATE: 2001-02-16
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                                                                                                       Sequence 13467, Application US/09815242 GENERAL INFORMATION:
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                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Matches 128; Conserv
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US-10-072-851-13467
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APPLICANT: ASALIA, SUCLIANT APPLICANT: Wall, Daniel APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, Robert T. APPLICANT: Boone, Charles APPLICANT: Boone, Charles APPLICANT: Boone, Charles APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Proliferation TITLE OF INVENTION: Proliferation FILE REPERBURE: BLITRA, 0.28A CURRENT APPLICATION NUMBER: US/10/072,851 CURRENT APPLICATION NUMBER: 60/267,636 PRIOR PELING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA, 0.28 VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITAA.028
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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;; Pred. No. 2.6e-15;
54; Mismatches 149;
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    PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                            ; ORGANISM: Staphylococcus aureus
US-09-815-242-5658
                                                                                                                                                                                                                                                                                                                                                                                           7 VGGLLFGLVYSPIVITGLHQSF---
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Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
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24.68;
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Best Local Similarity 24.65
Matches 111; Conservative
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US-10-072-851-5658
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APPLICANT:
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                                                                                                                                                                                                                                                                                                ----PPIELELFNQG---
                                                                                                                                                                                                                                                        Indels 137;
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                                                                                                                                                                                                         Length 679;
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APPLICANT: Carr. Grant J.
APPLICANT: Vamamoco. Robert T.
APPLICANT: Xu, H. Howard
APLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/103.21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2042,578
PRIOR APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                       17.1%; Score 310.5; DB 1
24.6%; Pred. No. 2.6e-15;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
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                                                                                                                                                                                                                                                                                                  7 VGGLLFGLVYSPIVITGLHQSF----
                                                                                                                  ; ORGANISM: Staphylococcus aureus PCT-US02-03987-5658
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Best Local Similarity
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APPLICANT:
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211 VAVFLEGEIKRLLIPFGLHHIFHAPFWFEFGSWKNAAGEIIHGDORIFIEOIREGAHLTA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 PITMEDDKDETVVVAEDKSATSELSHIVHAPLTGEVTPLSEVPDGVFSEKMMGDGIAIKP 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 296
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                                                                                                                                                                                                                                                                                                     448 ITRLRVEVNDKSKVDVPGLKDLGASGVLEVGNNMQAIFGPKSDQIKHEMQQIMNGQVVEN 507
                                                                                                40 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIFGVNL 95
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GENERAL INCORMATION:
APPLICANT: Haselbeck, Rari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Wall, Howard
TITLE OF INVENTION: Prokaryotes
FITLE OF INVENTION: Prokaryotes
FILE REFRENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PREDICATION NUMBER: 60/253,938
PRIOR FILING DATE: 2000-10-23
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12270
LENGTH: 681
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12270
7 VGGLLFGLVYSPIVITGLHQSF-
                                                                                                                                                                                                                                                                                                                                                                                                   166 LVR----
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GENERAL INFORMATION:
APPLICAMY: Elitra Pharmaceuticals, Inc.
APPLICAMY: Elitra Pharmaceuticals, Inc.
APPLICAMY: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of TITLE OF INVENTION: Proliferation
FILE REFERENCE: ElITRA, 028VPC
CURRENT FILING DATE: 2002-00-302
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 296
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                                                                                                                                                                                                                                                                                                                                                                                                           | ||| :| :| || || 3.00 VAVFLFGFIRKRLLIPFGLHHAPFWFEFGSWKNAAGEIIHGDQRIFIEQIREGAHLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 RLRWPFFIGIGTAAIGGALIALFNIKAVALG---AAGFLGVVSIDA-PDMVMF-----
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                                                                                                                                                                                                                                                                         17.1%; Score 310.5; DB 7;
24.6%; Pred. No. 2.6e-15;
Live 54; Mismatches 149;
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                  PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
PRIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                                                      ; ORGANISM: Staphylococcus aureus US-10-072-851-5658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12270
                                                                                                                                                                                                                                                                                                                                                                         7 VGGLLFGLVYSPIVITGLHQSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 LVCAVVTFFI------
                                                                                                                                                                                                                                                                                                   Best Local Similarity 24.6% Matches 111; Conservative
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Best Local Similarity 24.6
Matches 111; Conservative
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LENGTH: 681
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UGGLLEGLVGLYSPIVITGLHOSF	DKSKVDVPGLKDLGASG TTRAEAEAPAEFSNDS'	RESULT 10 PCT-USO2-03987-10089 Sequence 10089, Application PC/TUSO203987 GENERAL INFORMATION: TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Methods for Identifying the Target of a Compound FILE OF INVENTION: Methods for Identifying the Target of a Compound FILE OF INVENTION: MANBER: PCT_VUSO2/03987 CURRENT FILING DATE: 2002-02-02 PRIOR PAPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 15811 SOFTHARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10089 LENGTH: 648 TYPE: PRT TYP	Query Match       16.2%; Score 295; DB 1; Length 648;         Best Local Similarity 23.2%; Pred: No. 3.5e-14;         Matches 114; Conservative 62; Mismatches 162; Indels 154; Gaps 12;         QY 5 GPUGGLEFGLYSPIVITGLHQSPPI
Duery Match  17.1%; Score 310.5; DB 6; Length 681;  Bast Local Similarity 24.6%; Pred. No. 2.66-15;  Matches 111; Conservative 54; Mismatches 149; Indels 137; Ga 7 VGGLLFGLVSPIVITGLUGSF	Db 388 LVYAVIXYEVFRELIVKLKYKTPGREDKQSQAVTASATELPYAVLEAMGGRANIKHLDAC 447  Qy 166 LVRRNGSIDPD 176  ;	Oy 297 DEVKAGELLCEFDIDAIKAAGYEVTTPIVVS 327  Db 624 QEVKGGDLINFDLDXIRNHAKSDITPIIVT 654  RESULT 9 US-10-72-811-12270 ; Sequence 12270, Application US/10072851 ; GENERAL INFORMATION: ; APPLICANT: Carr, Grant J. ; APPLICANT: Carr, Grant J. ; APPLICANT: Anamudio, Carlos ; APPLICANT: Anamudio, Carlos ; APPLICANT: Application US/10072851 ; APPLICANT: Application US/10072851 ; APPLICANT: Trawick, John D. ; APPLICANT: Jang, Bo	TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of TITLE OF INVENTION: Proliferation FILE REFERENCE: ELITRA.028A US/10/072,851 CURRENT APPLICATION NUMBER: 05/267,636 PRIOR PAPLICATION NUMBER: 60/267,636 PRIOR PELLAG DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 15811 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 12270 LEWOTH: 681 TYPE: PRT TYPE: PRT ORGANISM: Staphylococcus aureus US-10-072-851-12270 Query Match Best Local Similarity 24.6%; Pred. NO. 2.6e-15;

DD 230 MSGFFPIMMFGLPGAALAMYFAAPKERRPMVGGMLLSVAVTAFLTGVTEPLEFLFMFLAP 289	Oy 92 GVNLRLEWPFFIGIGTAAIGGAL	Qy 115 IALFNIKA	Qy 129GFLGVVSIDAPDMVMFLVCAVVTFIAFGAAIAYG 163  Db 410 DACITRLITVADSARVNDTMCKRLGASGVVKLNKQTIQVIVGAKAESIGDAMKKVVARG 469	Qy 164 LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223  1	Qy 224 ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283	QY 284 LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343	RESULT 12 US-10-072-81-10089 ; Sequence 10089, Application US/10072851 ; GENERAL INFORMATION:	; APPLICANT: Carr, Grant J. ; APPLICANT: Xu, H. Howard ; APPLICANT: Foulkes, J. Gordon ; APPLICANT: Zamudio, Carlos ; APPLICANT: Uses heart Pobert	Ohlsen, Ke Zyskind, Wall, Dan Trawick,	,	; TITLE OF INVENTION: Methods for identifying the larger of a compound which inhibit, reference: ELITRA.028A ; CURRENT APPLICATION NUMBER: US/10/072,851 ; CURRENT FILMS DATE: 2002-02-08	; FRICK APPLICATION NUMBER: 50/26/036 ; NUMBER OF SEQ ID NOS: 15811 ; SOFTWARE: Fast-SEQ for Windows Version 4.0 ; SEQ ID NO 10089 ; LENGTH: 648	; TYPE: PRT ; ORGANISM: Escherichia coli US-10-072-851-10089	Query Match 16.2%; Score 295; DB 7; Length 648; Best Local Similarity 23.2%; Pred. No. 3.5e-14; Matches 114; Conservative 62; Mismatches 162; Indels 154; Gaps 12;	OY 5 GPVGGLLFGLVYSPIVITGLHOSFPPI
:  :  Db 350 IYFVVFSLVIRMFNLKTPGREDKEDEIVTEEANSNTEEGLTQLATNYIAAVGGTDNLKAI 409	Qy 129GFLGVVSIDAPDMVMELVCAVVTFFIAFGAAIAYG 163	QY 164 LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223  1	Oy 224 ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283	QY 284 LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343 	Oy 344 EAGANLINVAKK 355	RESULT 11 US-09-815-242-10089 ; Sequence 10089, Application US/09815242 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Robert ; APPLICANT: Ohlsen, Kari L. ; APPLICANT: Zyskind, Judith W.	Trawick, John D. : Trawick, John D. : Carr, Grant J. : Yamamoto, Robert T. : Xu, H. Howard	; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes ; FILE REPERENCE: ELITRA.011A ; CURRENT APPLICATION NUMBER: US/09/815,242 ; CURRENT PITING DATE: 2001.03-21	1	; FRIOR APPLICATION NUMBER: 60/20/,/2/ ; PRIOR FILING DATE: 2000-05-26 ; PRIOR FILING DATE: 2000-10-23 ; PRIOR FILING DATE: 60/253,625 ; PRIOR APPLICATION NUMBER: 60/253,625	FRIOR FILING DATE: 2000-11-2/ FRIOR PPLICATION NUMBER: 60/257,931 FRIOR FILING DATE: 2000-12-22 FRIOR APPLICATION NUMBER: 60/269,308 FRIOR FILING DATE: 2001-02-16	SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 10089  LENGTH: 648  TYPE: PRT  ORGANISM: Escherichia coli	%; Score 295; DB 6;	Best Local Similarity 23.2%; Pred. No. 3.5e-14; Matches 114; Conservative 62; Mismatches 162; Indels 154; Gaps 12;  Oy 5 GPVGGLLFGLYSPIVITGLHQSFPPI*	Db 170 GALGSGIFGFINRLIIPTGLHQVLNTIAWFQIGEFTNAAGTVFHGDINRFYAGDGTAGMF 229  Qy 43 IFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GITEPAIF 91

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----MVMFLVCAVVTFF-----
                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Enterococcus faecalis
PCT-US02-03987-10500
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith W.
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Matches 107; Conservative
                                                                  PCT-US02-03987-10500
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US-09-815-242-10500
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Hasing, Joseph E.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION X Sergei
FILE REFERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
                                                                                                                                                                                                                                 410 DACITRLRYADSARVNDTMCKRLGASGVVKLNKQTIQVIVGAKAESIGDAMKKVVARG 469
                                                                                                                                                                                                                                                                                                                                             ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283
                                                                                                                                                                                                                                                                                                                                                                 : : |:|| | |::| | |: : |: |:|| | |:||| | MSGFFPIMMFGLPGAALAMYFAAPKERRPMVGGMLLSVAVTAFLTGVTEPLEFLFMFLAP 289
                                                                                                                                                                                                         ---GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
                                                                                                                                                                                                                                                                          LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223
                                                                                                                                                                                                                                                                                                           470 -PVAAASAEATP-ATAAPVAKPQAVPNAVSIAE-----LVSPITGDVVALDQVPDEAF 520
                                                                                                                                                                                                                                                                                                                                                                                                                   LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343
                                                                                                                                                                     350 IYFVVFSLVIRMFNLKTPGREDKEDEIVTEEANSNTEEGLTQLATNYIAAVGGTDNLKAI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 PIGAALFGFFYAPLVITGVHQTTLAIDLQMIQSTGGTPIWPIIALSNIAQGSAVIGIIWA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                        290 LLYLLHALLTGISLFVATLLGIHAGFSFSAGAIDYALMYNLPAASQNVWMLLVMGVIFFA
                                                                                                                                       ------VALGAA-----
43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 276.5; DB 6 32.5%; Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Mismatches
                                                                  ---GVNLRLRWPFFIGIGTAAIGGAL---
                                                                                                                                     -----IALFNIKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRCANISM: Xenorhabdus sp.
US-09-897-516-6783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAGOTPLYEIKK 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 EAGANLLNVAKK 355
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Matches 54; Conserv
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US-09-897-516-6783
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APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 RLRWPFFIGIGTAAIGGALIALFNIKAVALG------AAGFLG-VVSIDAPD--- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| || |::| :| 244 PMMLVVQGLVFAAIYYFGFRFAITKFNLMTPGREEGDGEETPDVAEGDNKFASLARRIYD 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364 ADEMQRLYNHQAPATPVKETPVSQPVVEKKAPV--STKETELYSVANGKVIPISEVPDDV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 ----FATASMANIAQGAACLAVFFLAKSEKLKGLAG---ASGVSAVL-GITEPAIFGVNL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 551;
283 NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GPVGGLLFGLVYSPIVITGLHQSFPPI---ELELFNQGGSFI-
                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.0280FC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10500
                                                                                                                                                       ; Sequence 10500, Application PC/TUS0203987; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10500, Application US/09815242; GENERAL INFORMATION:
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304 GLGADANVTSIDNCTTRLRLTVKDTGKVDQAKIKATGVPGVKVIDDTNIQVIVGTEVQFV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 551;
## APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-34

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-12-17

PRIOR FILING DATE: 2001-12-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.2%; Score 276.5; DB 6; 23.0%; Pred. No. 6.8e-13; iive 68; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.04
Matches 107; Conservative
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Search completed: March 21, 2002, 16:27:37 Job time: 338 sec

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Sequence Sequence Sequence Bequence Beq
                                                                                                                                                                                                                                                                                Sequence 2
Sequence 1
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APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: MOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: -811A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
TELEPHONIS: 904-375-8100
TELEPHONE: 904-375-8100
             US-08-622-740-8

US-08-622-740-8

US-08-440-689-8

US-09-291-238-10

US-09-330-75-10

US-09-330-77-10

US-09-330-77-10

US-09-340-877-10

US-07-671-817A-5

US-08-349-867-19

US-08-349-867-19

US-08-349-867-19

US-08-349-867-19

US-08-349-867-19

US-08-340-857-19

US-08-39-305A-19

US-08-39-305A-19

US-08-598-305A-19
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STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/07828788A Patent No. 5273746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1176 amino acids
 CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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US-07-828-788A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
 Sequence 1, Appli
Patent No. 5164180
Patent No. 5189950
Sequence 3, Appli
Sequence 35, Appl
Patent No. 5254799
Sequence 7, Appli
Patent No. 5523211
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                (without alignments)
377.488 Million cell updates/sec
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Sequence 2, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 2, Appli
Sequence 12, Appl
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                                                                                                                               March 21, 2002, 16:23:16; Search time 21.58 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-463-308-7
US-08-836-325-2
US-08-446-486-6
US-08-157-363A-10
US-08-463-308-6
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US-08-933-891-2
PCT-US92-11337-12
US-08-040-751-1
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PCT-US93-11405-10
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US-08-836-325-12
US-08-674-351-2
US-08-836-325-15
US-09-413-814-70
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US-08-894-818B-35
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US-08-810-720-13
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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98.8
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COUNTRY:
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TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                         13;
                                                                                                      189 AEA-----EAP-----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 230
                                                                                                                                                                                     231 GVAIVPTKGQLVSPVSGKIVVAFPSCHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                               494 DILRITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
                                                                                                                                                                                                                                                                                                                         291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                549 ATMSSGGNLOSG------SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 593
                                           Gaps
                                                                               143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID------PDATAAPVPAG-----TTK 188
6.2%; Score 113.5; DB 1; Length 1176; 22.4%; Pred. No. 0.0076; tive 43; Mismatches 96; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/356,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/210,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/865,168
FILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08356034
Patent No. S691308
GENERAL INFORMATION:
GAPLICANT: Payne, Jewel M.
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                                         Conservative
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594 YIERIEFVPA 603
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                    Similarity
56; Conserv
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COUNTRY:
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Query Match
Best Local S
Matches 56
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Sequence 2, Application US/08933891
Patent No. 6096708
CENERAL INFORMATION:
APPLICANT: SICK, August J.
TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 AEA-----EAP----AEFSN---DSTIIOAPLTGEAIALSSVSDAMFASGKLGS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 DILRITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 593
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INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TW) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 113.5; DB 1;
22.4%; Pred. No. 0.0076;
tive 43; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                              ORGANISM: BACILLUS THURINGIENSIS
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 22.4%
Matches 56; Conservative
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CURRENT APPLICATION DATA:
                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM:
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594 YIERIEFVPA 603
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2: DAVID R. SALIWANCHIK
2421 N.W. 41st STREET, SUITE A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAYLD R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUINCATION INFORMATION:
TELEPHONE: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-040-751-1
'Sequence 1, Application US/08040751
'Patent No. 5407825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 12:
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Best Local Similarity 22.4%;
Matches 56; Conservative 4
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MOLECULE TYPE: protein
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                                                     GAINESVILLE
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 AEA-----EAP-----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
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GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.2%; Score 113.5; DB 3; Best Local Similarity 22.4%; Pred. No. 0.0076; Matches 56; Conservative 43; Mismatches 96;
                                                                                              FILING DATE: 09-APR-92
FILING DATE: 09-APR-92
FILING DATE: 09-APR-92
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
ATTORNEY, AGENT INFORMATION:
NAME: SALIWANCHIN, ROMAN REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/POCKET NUMBER: 21,023
REFEREN
                                                  US/08/210,110
US/08/356,034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER:
                                                  APPLICATION NUMBER:
                                                                             FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 ATMSSGGNLQSG---
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594 YIERIEFVPA 603
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HYPOTHETICAL: Y
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494 DILRITSPGQISTL---RVITTAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 ATMSSGGCLLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 113.5; DB 5; Length 22.4%; Pred. No. 0.0076; ve 43; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
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143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-----TTK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 596
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Length 1129;
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Patent No. 5188960

TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE

AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL

LEPIDOPTERAN-ACTIVE TOXINS

NUMBER OF SEQUENCES: 8

CURRENT APPLICATION NUMBER: US/07/451,261

FILING DATE: 14-DEC-1989

PRIOR APPLICATION NUMBER: 371,955

FILING DATE: 27-JUN-1989
                                                       Patent No. 5164180

APPLICANT: Payne, Jewel; Sick, August J.

TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106.5; DB 6;
Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.8%; Score 106.5; DB 6; Best Local Similarity 22.4%; Pred. No. 0.039; Matches 56; Conservative 42; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches
                                                                                                                                                                       APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
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Best Local Similarity 22.4%
Matches 56; Conservative
                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                  ; AGAINST LEPIDOPTERAN PESTS ; NUMBER OF SEQUENCES: 6
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597 YIDRIEFVPA 606
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5188960-2
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5188960-2
                                    5164180-6
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              APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
TITLE OF INVENTION: Lepidopteran-active Toxins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 ATMSSGGNLQSG------SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV
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                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113.3,
Pred. No. 0.0076;
                                                                                                                                                      ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 113.5; 22.4%; Pred. No. 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORREY/ACENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA39.C1.D3
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 NVAKKEAVPA 360
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597 YIERIEFVPA 606
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Matches 56; Conserv
GENERAL INFORMATION:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-040-751-1
                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL----FNQGGSFIFAT----ASMAN 51
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-894-818B-35
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                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                       552 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 596
438 SQAAGAVYTLRAPTFSWRHRSAEFSNLIPSSQITQIPLT-KSINLGSGTSVVKGPGFTGG 496
                                      231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                      497 DILRRISPGQISTL---RVIITAPLSQRYRVRIRY--ASTINLQFHISIDGRPINQGNFS 551
                                                                                                                            291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.5%; Score 99.5; DB 4; Length 522; Best Local Similarity 20.6%; Pred. No. 0.063; Matches 81; Conservative 63; Mismatches 114; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= Xaa at position 428 is Gly or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAKAKURA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                   TAKAKURA, Hikaru
MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITTA, Masanori
ASADA, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 amino acids
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                                                                                                                                                                                                                                           : 1 | 1 | 1 | 597 YIDRIEFVPA 606
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US-08-894-818B-3
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297 VNAYKAINYDNYAKLVFTGYVANKGS----QTHQFVI---SGASFVTATLYWDNANSDLD 349
                                                                                                     ---VNLRLRWPFFIGI-----GTAAIGGALIALFNIKAVALGAAGFLG--------- 132
                                                                                                                                                                                                                                                                      133 --VVSIDAPDMVMFLVCAVVTFFIAFG------AAIAYGLYLV--RRNGS-----ID 174
                                                                                                                                                                                                                                                                                                                                                                                           PDATAAP----VP--AGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSGVAI-----VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL 274
-----GASGVSAVLGITEPAI-----FG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MITHA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
APPLICANT: KATO, Ikunoshin
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 LYLYDPNGNQVDYSYTAYYGFEKVG----YYNP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 MHI--------GFDTVNLNGTHFNP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03253
FILLING DATE: 07-00v-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C. COUNTRY: United States of America
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SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSI 136
                                                                                                                    382 -GPNNQEFSVLDGTEF--SFASLTINPSTIYRORGTVDSLDVEIPPQDNSVPPRAGFSHR 438
                                                                                                                                                            -TTKAEAEAPAEFSN---DSTIIQAPLTGEAIALSSVSDAMFA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 -GPNNOEFSVLDGTEF--SFASLTINPSTIYRORGTVDSLDVEIPPQDNSVPPRAGFSHR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 MHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TTKAEAEAPAEFSN---DSTIIQAPLTGEAIALSSVSDAMFA 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGP 334
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                                                                                                                                                                                                                                                                  543 FHTSIDGRPINQGNFSATMSSGSNLQSG-----SFRTVGF--TTPF---NFSNGSS
                                                                             137 DAPDMYMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5254799

APPLICANT: DeGreve, Henri M. J.; Salgado, Maria B.L.; Van
Montagu, Marc C.E.; Vaeck, Mark A.; Zabeau, Maarcus F. O.; Leemans,
Jan J.A.; Hofte, Hermanus F. TITLE OF INVENTION: TRANSFORMATION VECTORS ALLOWING EXPRESSION
OF BACILLUS THURINGIENSIS ENDOTOXINS IN PLANTS

NUMBER OF SEQUENCES: 42
                                         --RRIILGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1188;
                                                                                                                                                                                                  439 LSHVTMLSQAAGAVYTLRATFSWQHRSAEFNNIIPSSQITQIPLT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 SPVGFSGPEFAFP----LFGNAGN----AAPQORIAGNAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/555,828
FILING DATE: 23-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 821,582
FILING DATE: 22-JAN-1986
APPLICATION NUMBER: 692,759
FILING DATE: 18-JAN-1985
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                                     ----PVLSLTGLGIFRT---LSSPLY----
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5254799-7
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5254799-7
                                                                                                                                                            186
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                                                                                                                                                                                                                                                                                                      260 IKVINLSL-----GSSQSSDGTDALSQAVNAAWDAGLVVVVAAAGNSGPNKYTIGSPAAA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                             .- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 DYYTAAPGTSMATPHVAGIAALLLQAHPSWTPDKVKTALIETADIVKPDEIADIAYGAGR 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDATAAP-----VP--AGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGSGVAI------VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL 274
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                               1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL----FNQGGSFIFAT----ASMAN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 SPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGA 76
                                                                                                                                                                                                5.5%; Score 99.5; DB 4; Length 654;
20.6%; Pred. No. 0.089;
Live 63; Mismatches 114; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DeGreve, Henri M. J.; Salgado, María B.L.; Van, Montagu, Marc C.E.; Vaeck, Mark A.; Zabeau, Maarcus F. O.; Leemans, Jan J.A.; Hofte, Hermanus F. P. TITLE OF INVENTION: TRANSFORMATION VECTORS ALLOWING EXPRESSION: OF BACILLUS THURINGIENSIS ENDOTOXINS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 127; Indels 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VNLRLRWPFFIGI----GTAAIGGALIALFNIKAVALGAAGFLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%; Score 98; DB 6
19.9%; Pred. No. 0.33;
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FILING DATE: 23-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 821,582
FILING DATE: 22-JAN-1986
APPLICATION NUMBER: 692,759
FILING DATE: 18-JAN-1985
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              SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                       81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                    Similarity
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Best Local Similarity
Matches 77; Conserv
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;Patent No. 5254799
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5254799-6
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                                                                                                                                                                                                Query Match
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                                                                                     1756 FVSYIIISFLVVVNMYIA----VILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDAT- 1810
1697 FETFGNSMICLFQITTSA-GWDGLLAPILNSGPPDCDPEKDHPGSSVKGDCGNPSVGIFF 1755
                                                                                                                                                                            1811 ------QFIEFCKLSD--FAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAF 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 ISTLRVNITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSG-535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA-----EAP-----AE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 FSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP----TKGQLVSPVSG-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 ----KIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 LLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 FLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTI
                                                                                                                                   204 IQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS----PVSGKIVVAFPSGHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IDENTIFICATION, QUANTITATION AND PURIFICATION OF INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSECTICIDAL COTTON PLANTS (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                               5523211-1
;Patent No. 5523211
; APPLICANT: PUSZTAI-CAREY, MARIANNE;CAREY, PAUL R.; LESSARD,
                                                                                                                                                                                                                                               1862 TKRVLGESGEMDALRIQMEERFMASNPSKVSYEPITTTLKRKQEEVSA 1909
                                                                                                                                                                                                                        260 AVRTKAEDG--SNVDILMHIGFDTVNLNGTHFNP----LKKQGDEVKA 301
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0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.3%; Score 96.5;
22.4%; Pred. No. 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/277,076
FILING DATE: 19-7UL-1994
PRIOR APPLICATION NUMBER: 102,491
FILING DATE: 19-FBB-1992
APPLICATION NUMBER: 836,967
FILING DATE: 19-FBB-1992
APPLICATION NUMBER: 493,453
FILING DATE: 14-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Nicholas J. Seay
One South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08810720
Patent No. 6037527
GENERAL INFORMATION:
APPLICANT: Barton, Kenneth A.
TITLE OF INVENTON: INSECTICIDAL CO
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nicholas J. Seay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.48;
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Best Local Similarity
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                                                                                                                                                                                                                                                          APPLICANT: Mandel, Gail
APPLICANT: Malegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --MVM 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 LKGLAGASGVSAV---LGITEPAIFGVNLRLRWPFFI----GIGTAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                           335 VNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                         589 VFTLSAHVFNSG-NEVYIDRIEFVPA 613
                                                                                                                                                                                              Sequence 7, Application US/08836325
Patent No. 6110672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 2005 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-836-325-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: DC
STATE: DC
COUNTRY: USA
TO: 20005-3934
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Matches 64; Conserva
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
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STREET: 110
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completed: March 21, 2002, 16:23:18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1.934
CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-446-486-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
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hes 53; Conserv
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Job time:
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APPLICANT: De Greve, Henri Marcel J
APPLICANT: Salgado, Maria Benita Leonor F
APPLICANT: Vaeck, Mark A
APPLICANT: Vaeck, Mark A
APPLICANT: Zabeau, Marcus Florent O
APPLICANT: Leemans, Jan Jozef A
APPLICANT: HOffe, Hermanus Fransiscus P
APPLICANT: Hoffe, Hermanus Fransiscus P
APPLICANT: HOffe, Hermanus Fransiscus P
TITLE OF INVENTION: EXPRESSION OF FOREIGN POLYPEPTIDE ENDOTOXINS FROM BACILLUS
TITLE OF INVENTION: THURINGIENSIS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA-----EAP-----AE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 FSN----DSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP----TKGQLVSPVSG-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 FNNIIPSSQITQIPLT------KSTNLGSGTSVVKGPGFTGGDILRRTSPGQ 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 ISTLRVNITAPLSQRYRVRIRY -- ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 LLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.3%; Score 96.5; DB 3; Length 648; Best Local Similarity 22.4%; Pred. No. 0.18; Matches 53; Conservative 33; Mismatches 78; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Burns, Doane, Swecker & Mathis
George Mason Bldg., Washington & Prince Sts
                                                                                  OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/810,720
FILING DATE: 03-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 670513.90163
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-9166
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08446486
Patent No. 5545565
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 648 amino acids
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COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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ADDRESSEE: Burns, Do
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COMPUTER READABLE FORM:

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166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA-----EAP-----AE 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "deduced amino acid sequence
of B.t. sotto (Shibano et al., Gene 34, p. 243,
1985)"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 06/692,759
FILING DATE: 18-JAN-1985
ATTONNEY, AGGNT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-047
TELECOMMINICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/133,965
FILING DATE: 08-0CT-1993
APPLICATION UNBER: US 08/014,148
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 06/821,582 FILING DATE: 22-JAN-1986 PRIOR APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/555,828 FILING DATE: 23-JUL-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 934 amino acids
amino acid
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13;

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(without alignments)
629.745 Million cell updates/sec
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1821
1 YDFGGPVGGLLFGLVYSPIV......IEAGANLLNVAKKEAVPATP 362
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/SIDSB/gcgdata/geneseg/genesegp/AA1990.DAT:*
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/SIDSB/gcgdata/geneseq/genesegp/Aal985_DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	C.qlutamicum phosp	C.qlutamicum phosp	C glutamicum prote	Brevibacterium lac	C qlutamicum prote	C.qlutamicum phosp	Escherichia coli p	C.glutamicum phosp	B. burgdorferi ant	Amino acid sequenc	B. burgdorferi ant
	ΩI	1	AAB66707	AAG92650	AAB69080	AAG93207	AAB66721	AAG98282	AAB66723	AAY20012	AAY53620	AAY20013
	8	22	22	22	22	22	22	22	22	20	21	70
	Query Match Length DB	362	468	661	661	683	683	648	135	167	583	135
	Query	100.0	100.0	100.0	99.5	21.4	21.4	16.2	12.9	12.8	12.2	9.1
	Score	1821	1821	1821	1806	390.5	390.5	295	234	233.5	221.5	166.5
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Amino acid sequenc Human ORFX ORF555 Streptococcus pneu C glutamicum prote Delta endotoxin. Human adult form o	001	C glutamicum prote Amino acid sequenc T. halophilus xyul C glutamicum prote Peptide #1570 enco Peptide #1628 enco	Peptide #1559 enco Peptide #2757 enco Human adult form o Streptomyces globi Streptomyces globi P. denitrificans CO C. glutamicum SRT C. glutamicum prote	Hyperthermostable Pyrococcus furiosu Hyperthermostable Pyrococcus furiosu Hyperthermostable Rat multidrug resi Rat multidrug resi Enterococcus faeca Human adult form o
AAW28051 AAB40791 AAY81556 AAG90449 AAR39755 AAB99678	AAB99679 AAY21797 AAY21796 AAR08258	AAG91953 AAW59912 AAW58862 AAG90809 AAM15136 AAM27591	AAM02877 AAM04075 AAB199674 AAB13578 AAB13605 AAB13498 AAB78983 AAG92907	AAW94836 AAW94838 AAW94838 AAW94841 AAY70596 AAY70597 AAY70597 AAY00194
18 21 22 14 22	25 20 11 11 11	755 755 755 755 755 755 755 755 755 755	22222222	70 70 70 70 70 70 70 70 70 70 70 70 70 7
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12 13 14 16	18 19 20 21	22 2 2 3 3 3 4 4 3 3 3 4 4 3 3 3 4 4 4 3 3 3 4 4 4 3 3 4	12 w w w w w w c 0 0 0 4 0 4 0 0 1	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

RESULT

Schroeder H, Zelder O, Haberhauer G; Phosphoenolpyruvate; sugar phosphotransferase system; PTS C.glutamicum phosphoenolpyruvate protein #2. AAB66708 standard; protein; 362 AA. 99US-0142691. 99US-0150310. 99DE-1042095. 99DE-1042097. 27-JUN-2000; 2000WO-IB00973. Corynebacterium glutamicum 09-APR-2001 (first entry) Pompejus M, Kroeger B, WPI; 2001-080989/09. (BADI ) BASF AG. WO200102583-A2 23-AUG-1999; 03-SEP-1999; 03-SEP-1999; 01-JUL-1999; 11-JAN-2001. AAB66708; AAB66708 

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers

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Corynebacterium glutamicum
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          (BADI ) BASF AG
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                                 The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
                                                                                                                                                                                                                                  121 KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA 180
                                                                                                                                                                                                                                                                       240
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                                                                                                                                               100.0%; Score 1821; DB 22;
100.0%; Pred. No. 6.5e-171;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.glutamicum phosphoenolpyruvate protein #1.
                  Page 104-106; 144pp; English.
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99US-0150310.
99DE-1042095.
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                                                                                                                                                                  Conservative
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for transformation
                                                                                                                                                         Local Similarity
                                                                                                                      362 AA;
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
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       Haberhauer
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ilarity 100.0%; Pred. No. 9.4e-171;
Conservative 0; Mismatches 0; 1
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                                                                                                                                                                                                                              Claim 4; Page 101-102; 144pp; English.
     Schroeder H,
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA 180
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Pred. No. 1.6e-170;
Wismatches 0;
                                                                                                                                                                                    H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                        16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                           18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 362; Conservative
                                                                                                                                                                                    Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Patent Office
                                                                                                                                                                                                                               2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 AA;
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EP1108790-A2
                                                                                                                                                                                    Nakagawa S,
Tateishi N,
                              20-JUN-2001
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The present sequence represents the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and have improved amino-acid and nucleic acid productivity.
                                                                                                                                               Brevibacterium lactofermentum sucrose PTS enzyme II protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzym
II obtained by cassette ligation-mediated amplification of downstream
domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                        Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system.
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Pred. No. 4.7e-169;
2; Mismatches 1;
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  Ā
AAB69080 standard; Protein; 661
                                                                                                                                                                                                                                                                                            Brevibacterium lactofermentum
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                                                                                              (first entry)
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Matches 359;
                                              AAB69080;
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307 ivipllypflvplglhwplnaimignintlgydfiggpmgawnfacfglvtgvfllsike 366
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                                                                                                                                      KLKGLAGAS--GVSAVL--GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA
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30.7%; Pie.
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99US-0150310.
99DE-1042095.
99DE-1042097.
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                Local Similarity 30.7% nes 118; Conservative
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23-AUG-1999;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                241 LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK 300
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            pvpagttkaeaeapaefsndstiiqapltgeaialssvsdamfasgklgsgvaivptkgg
                                                                  Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid synthesis; vitamin; saccharide;
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da M, Ozaki A;
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Senoh A, Ikeda M,
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organic acid synthesis.
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03-AUG-2000;
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Tateishi N,
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NOT COURT OF 
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the
ö
Haberhauer
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Schroeder H, Zelder
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identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID------
                                                                                                                                                                                                                                                                  Length 683
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                            21.4%; Score 390.5; DB 22; 30.7%; Pred. No. 1.3e-29; iive 60; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli protein sequence SEQ ID NO:330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US34419
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Best Local Similarity 30.79
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-457376/49.
N-PSDB; AAH81338.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2001
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                                                                                                                                                                              Sequence
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12;
                                                                                             The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences yetven in AAA881202 to AAH881294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for Xilling bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as day according to the proliferation can be used as day of the proliferation.
                                                                                                                                                                                                                                                                                                                                                                 For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coll proteins given in AAG88239 to AAH81481, and AAH81488 to AAH81491 represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 iyfvvfslvirmfnlktpgredkedeivteeansnteegltqlatny1aavggtdnlkai 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ELELFNQG----GSF 42
Novel nucleic acids encoding proteins required for Escherichia coli proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%; Score 295; DB 22; 23.2%; Pred. No. 3e-20; ive 62; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GVNLRLRWPFFIGIGTAAIGGAL----
                                                             Claim 19; Page 462-463; 596pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.2
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 EAGANLLNVAKK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 AA;
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Query Match 12.0%;
Best Local Similarity 34.8%;
Matches 46; Conservative
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                                                                                                                                                                                        (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 GPVNTYGLGEIE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 ssie-ysfgrle 127
                                Borrelia burgdorferi.
                                                                                                                                                                                                                                  WPI; 1999-189980/16
                                                                                                                                                                                                                                                                                                                                                                                                                           167 AA;
                                                                                                                                                                                                                                              N-PSDB; AAX61709
                                                      WO9859071-A1
                                                                                                 18-JUN-1998;
                                                                                                                                20-JUN-1997;
                                                                                                                       03-SEP-1997;
                                                                                                                                                        22-JUL-1997;
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                                                                            30-DEC-1998
                                                                                                                                                                                                              Choi GH,
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                                                                                                                                                                                                                                                                                                                        sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation
                                                                                                                                                                                                                                                                                                                                                                                                  phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 DAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | | | | : :||||: | || | |: : ||:|||| | |: 58 dtvqlggegftvhverrgqvkagdplitfdadfirskdlplitpvvvsnaakfgeiegip 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 DTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYG 339
                                                                                                                                                                                                                                                                                                            Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate:
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                                                                                                                                                                                                                                                                   Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to Corynebacteium glutamicum
                                                                           Phosphoenolpyruvate; sugar phosphotransferase system; PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.9%; Score 234; DB 22; Best Local Similarity 37.5%; Pred. No. 3.1e-15; Matches 51; Conservative 25; Mismatches 56;
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                                                                                                                                                                                                                                                                   Zelder
                                                     C.glutamicum phosphoenolpyruvate protein #7.
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                                                                                                                                                                                                                                                                                                                                                                   Claim 36; Page 142-143; 144pp; English.
                                                                                                                                                                                                                                                                   Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY20012 standard; Protein; 167
                                                                                                                                                                                      99US-0142691.
99US-0150310.
99DE-1042095.
99DE-1042097.
                                                                                                                                                                 27-JUN-2000; 2000WO-IB00973
                                                                                                 Corynebacterium glutamicum
                               (first entry)
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                                                                                                                                                                                                                                                                 Kroeger B,
                                                                                                                                                                                                                                                                                      WPI; 2001-080989/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AA;
                                                                                                                                                                                                                                            (BADI ) BASF AG.
                                                                                                                      40200102583-A2
                                                                                                                                                                                                 23-AUG-1999;
03-SEP-1999;
                                                                                                                                                                                                                        3-SEP-1999;
                                                                                                                                                                                                                                                                   Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-1999
                                                                                                                                                                                      01-JUL-1999;
                               09-APR-2001
                                                                                                                                            11-JAN-2001
          AAB66723;
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This sequence represents a Borrella burgdorfer! (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrella genus, particularly for the use against Lyme disease in memors and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrella genus. The products can also be used for detection of members of the Borrella genus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 IALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a permease encoded by the lactose operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n,
Antigenic protein; vaccine; Lyme disease; infection; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactose operon; permease; beta-galactosidase; mutant; yoghurt; beta-galactosidase activity; lactose fermentation; fermented milk product; Streptococcus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 233.5; DB 20; 34.8%; Pred. No. 4.7e-15; ive 30; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lathigra R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY53620 standard; Protein; 583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 161; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erwin AL, Hanson MS,
                                                                                                                                                                                                                                                                                                                                                                              97US-0050359.
97US-0053344.
97US-0053377.
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AAW28051 standard; Protein; 126 AA.
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                                                                                                                                                                 AAY20013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi
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                             300
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AAW28051
ID AAW2
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                                                                                                                                                                                                                                                                                                                           AAY53620-21 are encoded by the lactose operon of Lactobacillus bulgaricus, and represent a permease (AAY53620) and beta-galactosidase AAX53621). The specification describes a mutant L. bulgaricus strain lacking beta-galactosidase activity, because it has a termination (nonsense) mutation in at least one of the coding sequences of the factose operon. The resulting mutant strain is unable to ferment lactose produced using it do not have to be cooled to prevent post-acidification. The mutant L. bulgaricus strain of the invention is used for producing a fermented milk product, especially yoghurt. Especially, milk is fermented with a culture of the mutant strain and optionally Streptococcus thermophilus in the presence of at least one sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                        New mutant Lactobacillus bulgaricus strain lacking beta-galactosidase activity useful for making fermented milk products, especially yoghurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 lvgaefffipgplaflvvlmiisdaveygqlktghrdealtlsvrplvdklggalsnwfv 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 thevksalresnekttlkgvfkvlggndgllwlafaywfyglgintlnalglyyfsyilg 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFGG-----PVGGL-LFGLVYSPIVI-----TGLHQSFPPIELE------LFNQGGS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LGVVSIDAPDMVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITEP------AIFGVNLRLRWPFF-----IGIGTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%; Score 221.5; DB 21; Length 21.8%; Pred. No. 4.4e-13; Live 66; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assimilable by the mutant strain, preferably glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVCAVVTFF---IAF----GAAIAYG----
                                                                                                                                                                                                                                                                                                     French.
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                                                                                                                                                                 Gendre F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AIGGALIALFNIKAVALGAAGF--
                                                                                                                                                                                                                                                                                                     Disclosure; Page 22-24; 32pp;
                                                                                                                                  (DANO-) CIE DANONE SA GERVAIS
                                                                         98FR-0006456.
                                                                                                    98FR-0006456.
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                                                                                                                                                                Brignon P,
                                                                                                                                                                                            WPI; 2000-026146/03.
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Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 AA;
                                                                                                                                                                                                            N-PSDB; AAZ36227
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            FR2778921-A1
                                                                        22-MAY-1998;
                                                                                                    22-MAY-1998;
                                                                                                                                                                Benbadis L,
                                          26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GKIVVAFFSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 306
469 kvyapfagtvrqlaktrhsivl----enehgvlvlihlglgtvklngtgfvsyveegsqv 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a Borrelia burgdorferi (Bb) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to develop
diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166.5; DB 2
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lathigra R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi antigenic protein, t346.aa
                                                                          :||::|| |||| |:| |:| || 553 eaggqilefwdpaikqaklddtvivtvin 553
                                                  KAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
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                                                                                                                                                                                                                               AAY20013 standard; Protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
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97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-189980/16.
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Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Staphylococcus aureus protein, that, based on homology with a human or Staphylococcus aureus protein, is believed to be a nerve growth factor or ptsG protein. The DNA sequence was isolated from a library of clones of S. aureus WCHH 29 in Escherichia coll. The DNA sequence can be used in the construction of riboxymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The prosent protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host dagminst invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                               //octe= "residues designated X are not defined in
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S.
                                                                                Amino acid sequence of Staphylococcus aureus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knowles DJC,
Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Pages 432-433; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberg M,
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMIK ) SMITHKLINE BEECHAM CORP.
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                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burnham MK,
Reichard RW,
                                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                    coxic shock syndrome.
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                                                                                                                                                                                                                                                   Misc-difference 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus infection
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                                               27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                     21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pratt JM,
               AAW28051;
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidlabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; ontiviral; antifungal; antirheumatic; antihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder uncleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 LGSGVAI-VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 THFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAG 346
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                 DB 18; Length 126;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                            8.9%; Score 161.5; DB 132.8%; Pred. No. 3.8e-08;
Live 25; Mismatches 44
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                     Matches
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useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease

Claim 11; Page 1038; 5507pp; English.

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitinacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malarial; autofmmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                   Human ORFX ORF555 polypeptide sequence SEQ ID NO:1110.
                        AAB40791 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2000; 2000US-0540763
                                                                         (first entry)
                                                                                                                                                                                                                                                                                              thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1999;
05-APR-1999;
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                                                                         08-FEB-2001
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          AAB40791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                  194 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 253
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                           4;
                                                                                                                                                      8.5%; Score 154; DB 21; Length 108; 32.7%; Pred. No. 1.7e-07; tive 19; Mismatches 43; Indels
to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae type 4 protein sequence #56.
                                                                                                                                                                                                                                                                                                                                                                                                                                            254 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY81556 standard; Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIAL TECHNICS LTD.
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99US-0125164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal disease.
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                                                                                                                                                                                    Best Local Similarity
Matches 32; Conserv
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                                                              108 AA;
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coagulation;
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                  94 NLRLRWPFFIG-IGTAAIGGALIALFNIKAV-----ALGAAGFLGVVSIDAPDMVMF 144
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                                                                VGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATAS----MANIAQGAA----
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                              57;
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Tateishi N, Senoh A, Ikeda M, Ozaki A;
        3e-06;
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                              Mismatches
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26.78; Pic
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum.
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                              Conservative
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              Local Similarity
les 56; Conserv
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                                                                                                                                                                                                  -----GVSAVLGITEP 88
                                                                                                                                 7 VGGLLFGLVYSPIVI----TGLHQSF-----PPIELELFNQGGSFIFATASMANIAQG- 55
                                                                Query Match 6.5%; Score 118.5; DB 22; Length 805; Best Local Similarity 22.8%; Pred. No. 0.0099; Matches 101; Conservative 55; Mismatches 174; Indels 113;
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Tetraodon

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602418142 Drosophil

EST391869 EST391888 EST483354 EST483628 EST484167 EST485382

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AW173566 AI917973

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Drosophil Drosophil

14-FEB-1997

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CDNA clone FB20C8, mRNA
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Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Sep 21, 1992 this sequence version replaced gi:279156. Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="ATCC (inhost):86662"
/db_xref="GDB:D052785E"
/db_xref="taxon:9606"
/clone="FFB20C8"
/clone="FFB20C8"
                                                                                                                                                                                                                                                                                                                                                                                                       T03017 473 bp mRNA EST FB20C8 Fetal brain, Stratagene Homo sapiens
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                                     CNS0021D
CNS025EN
AW573719
BE998387
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T03017.1 GI:314258
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COMMENT
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T03017/c
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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/note="Vector: Lambda ZAP II; The FB library (catalog #937201, Stratagene) was constructed by directional coloning and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 681)

1 (bases 1 to 681)

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2 (bases 1 to 681)

Weissenbach.L. Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
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g 282 t 50 others
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/clone="262H14"
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/organism="Tetraodon
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/clone_lib="G"
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ilarity 59.7%;
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                214 ggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagcctgcgatcttc 273
                                                                                                                                                                  274 ggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcggtaccgcagctatcggt 333
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                                                                   Gaps
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                                                                                                                                                                                                                                                                                                   178 GINGITGITGINGCCGINGITGITGCYGTTGITGITTTTTGITGITGTTGTTGTTGTTGTTGTT
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Length 681;
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/db_xref="taxon:7227"
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   DB 13;
                                                                18; Mismatches 183;
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Score 41.8; DE
Pred. No. 1.3;
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/clone="BACR14B09"
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
VII Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 477)
Fedorova,M., Plerson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTS from sensescent nodules of Medicago truncatula
Unpublished (2000)
Contact: Carroll P. Vance
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                                                                                      gggtgcggcatgtttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgc 221
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                                            Gaps
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                                                                                                                                                                                                                                                                               Email: varce004@maroon.tc.umn.edu
University of Minnesota name: M271936e TIGR sequence name:
MTKAK05TKB More information is available at:
                                            ö
      Length 895;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE997958 477 bp mRNA EST
EST429681 GVSN Medicago truncatula cDNA clone
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3.8%; Score 41.6; DB 13;
1larity 19.9%; Pred. No. 1.6;
Conservative 115; Mismatches 159;
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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/clone_lib="GVSN"
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Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Peng, H. Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, J.E. and Fraser, C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: Shoi; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Glappack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Tel: 612 625 5715
Fax: 651-649-5058
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EST316674 GVN Medicago truncatula cDNA clone pGVN-51G2, mRNA
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Pred. No. 1.6;
); Mismatches 101;
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Department of Agronomy and Plant Genetics
University of Minnesota
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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TIGR sequence name:MTCAR37TK
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University of Minnesota name: M381580e TIGR sequence name:
MTCC740TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA AAA CTA gtg gAT CC).
Location/Qualifiers
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EST482254 GVN Medicago truncatula cDNA clone pGVN-57H8 5' end, mRNA
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Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                          inoculation with Sinorhizobium meliloti. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
/tissue_rype="NX-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab.host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: ECORI; Site_2:
XhoI; CDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
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Pred. No. 1.6;
0; Mismatches 101; Indels 0
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Unpublished (2001)
Contact: Carroll P. Vance
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Best Local Similarity 50.2%;
Matches 102; Conservative
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Medicago truncatula
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/organism="Medicago truncatula"

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/issue_type="No-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inculation with Sinorhizoblum meliloti"
/lab_host="E. coll strain XLOLR"
/lab_host="E. coll strain XLOLR"
/lab_host="E. coll strain XLOLR"
/note="Vector: pBluescript SK-; Site=1: ECORI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Glappack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
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C.D., Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
C.D. senescent nodules of Medicago truncatula
Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Fax: 651-649-5058
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Eukaryota, Vildiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Pabales, Fabaceae, Papillonoideae, Trifolleae,
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MTRAP54TK More information is available at:
http://chrysie.tamu.edu/medicago
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Location/Qualifiers
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50.2%; Pred. No. 1.7;
tive 0; Mismatches 101;
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-57H8"
/clone_lib="GVN"
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/clone_lib="GNS"
/clone_lib="GNS"
/clone_lib="GNS"
/clone_lib="GNS"
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/clone_lib="GNS"
/clone_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coll strain SOLR"
/lab_host="E. coll strain SOLR"
/note="Wector: pBluescript SK +/; Site_l: ECORI; Site_2:
XhoI; CDNA was prepared from polyk+ enriched RNA from the mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The collected from 2 month old plants at mid-pod stage. The CDNA was directionally ligated into the Uni-ZAP XR vector from Strategene and packaged using Glapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley brosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information pleases see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N21 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 1.7;
0; Mismatches 101;
                  /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVSN-9112"
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983 bp DNA GSS 15-MAY-2000 nigroviridis genome survey sequence PUC-Or1 end of clone library G from Tetraodon nigroviridis, genomic survey
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1 (bases 1 to 983)

1 (bases 1, Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcosI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          329 others
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/db_xxef="laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 15.0%; Pred. No. 2.7;
Conservative 147; Mismatches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%; Score 40.8; DF 15.0%; Pred. No. 2.7;
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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BSTs from senescent nodules of Medicago truncatula
Unpublished (2000)
Contact: Carroll P. Vance
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Stakaryota; Viridipliantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST429680 GVSN Medicago truncatula cDNA clone pGVSN-8B9, mRNA
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                      3 (bases 1 to 970)
Genoscope
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
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University of Minnesota
University of Minnesota
11 Borlauq Hall, 1991 Upper Buford Circle, St.Paul, MN 55:
Tel: 612 625 5715
Fax: 651-649-5058
Email: wance004@marcon.tc.umn.edu
University of Minnesota name: M71935e TIGR sequence name:
MTKAK05TK More information is available at:
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/organism="Tetraodon nigroviridis"
/db_xref="Laxon:99883"
/clone="026011"
/clone_lib="G"
/note="Genoscope sequence ID : COB
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4;
2; Mismatches 151;
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BE997957.1 GI:10698233
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Best Local Similarity 45.9%;
Matches 130; Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Necteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.
I (bases 1 to 970)
Roest-Crollius, H., Jaillon, O., Dasilva; C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Barnin, W. and Weissenbach, D. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis genome survey sequence T7 end of clone
026011 of library G from Tetraodon nigroviridis, genomic survey
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="015D07"
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53.0%; Pred. No. 2.7;
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                                                                                                                                                                                      /issue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-: Site_i: EcoRI: Site_2: XhoI; cDNA was prepared from polyA+ enriched.RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Giapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist Helper phage and propagated in SOLR cells."
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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BACR27802 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL067821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 CAATGAAGAAGTGAGCGACTTTGTTCGTGAGGCTGATTCTGATAGTGATGGACATCTAAG
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http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6%; Score 39.8; DB 11; 49.8%; Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 102;
                                                                                     /organism="Medicago truncatula"
                                                                                                         /cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                    /clone="pGVSN-8B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1008 cacttacggtttgggcgaaattg 1030
                                                                                                                                                                           /clone_lib="GVSN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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VERSION
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The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Eye library. CDNA Library Preparation: M. Fatima Bonaldo. Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRi digestion of Drosophila DNA provided by the BDGP from the lisogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 539)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 gcctgcgctggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgattg 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 cactetttaatateaaggeagttgegttgggegetgeaggtttettgggtgttgttteta 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 ttgatgctccagatatggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcat 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIO70146 539 bp mRNA EST 05-JUL-1999 UI-R-Y0-lu-g-12-0-UI.s1 UI-R-Y0 Rattus norvegicus CDNA clone UI-R-Y0-lu-g-12-0-UI 3', mRNA sequence.
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451 Eckstein Medical Research Building Iowa City, IA 52242,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 993;
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db.xxef="laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR23F02"
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Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39.2; DB 13;
Pred. No. 7.4;
1; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 teggegeagegattgettatggeetttaettggtt 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
97044477
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 104; Conserve
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// ACLE="Vector: pr73D-pac (Pharmacia) with a modified polylinker: SITE_1: Not I; Site_2: Eco RI: The UI-R-YO Ibrary is a subtracted ilbrary derived from an individually-tagged normalized whole-eye (minus the lens) individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO, UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted ilbrary (UI-R-YO) was constructed as follows: PCR amplified CDNA inserts from previous library clones from which 3' ESTS had been derived were used as a driver in a whole-eye library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-YO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AWS83970 714 bp mRNA EST 05-JUL-2001 ia07h02.x1 Human Pancreatic Islets Homo sapiens CDNA 3' similar to SW.RL14_HUMAN P50914 60S RIBOSOMAL PROTEIN L14 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 714)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID-1785384 The following repetitive elements were found in this cDNA sequence: 357-476, >(CAA)n#Simple_repeat 478-538, >(CAA)n#Simple_repeat Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 teggtateggtacegeagetateggtggegetttgattgeaetettaatateaaggeag 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 ttgcgttggggcgctgcaggtttcttgggtgttgtttctattgatgctccagatatggtca 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 ITGTTGTTATTTCTGTTGTTGTTGTTGTTGCTGCTGTTGTTGTTATTTCTGTTGTTG 402
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Pred. No. 8.2;
0; Mismatches 87; Indels 0
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                                                                                                                                                                                                                                                                                                                           /clone="UI-R-Y0-lu-g-12-0-UI"
/clone_llb="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley'
/db_xref="taxon:10116"
                                                                                                                                                                              Location/Qualifiers
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KEYWORDS
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Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation;
                                                                                                                                                                                                         Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                            Library was constructed by Dr. Douglas Melton DNA sequencing by: washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
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                                                                                                               Unpublished (2000)
Other_ESTs: ia07h02.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH108"
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3.5%; Score 38.8;
Best Local Similarity 47.2%; Pred. No. 8.6
Matches 118; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 714
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                         Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 304.
Location/Qualifiers
                                                                                                                                                                                    Endocrine Pancreas Consortium
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                                                          Contact: Steven A. Williams
Milliams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes aspressed in molting L3 larvae of Onchocerca volvulus Genes aspressed in molting L3 larvae of Onchocerca volvulus Gontact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853786
Fax: 4135853786
Email: genome@smith.edu
                                Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                           /organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                 /clone="SWOv3MCAM11A12"
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Location/Qualifiers
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102 c 56 q
                                              Onchocercidae; Onchocerca.
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